

GenCore version 5.1.6
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OM protein - protein search, using sw model
Run on: June 3, 2004, 08:53:00 ; Search time 17 Seconds
(without alignments)
744.297 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281
Perfect score: 1287
Sequence: 1 TNELKQMDKYSGIACFL.....NEHLIDMDHEASFGAFLVG 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070455 residues 141681
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1287	100.0	281	1 TN10_HUMAN	P50591 homo sapien
2	863	67.1	291	1 TN10_MOUSE	P50592 mus musculus
3	250.5	19.5	318	1 TN11_RAT	Q95922 r tumor nec
4	238.5	18.5	316	1 TN11_MOUSE	Q35235 m tumor nec
5	235.5	18.3	317	1 TN11_HUMAN	O14788 h tumor nec
6	189.5	14.7	279	1 TNF6_MOUSE	P41047 mus musculus
7	185.5	14.4	280	1 TNF6_CERVO	Q9bdn1 cercocebus
8	183.5	14.3	280	1 TNF6_MACMU	Q9my16 macaca mula
9	182.5	14.2	281	1 TNF6_HUMAN	P48023 homo sapien
10	182	14.1	282	1 TNF6_PIG	Q9bea8 sus scrofa
11	177.5	13.8	278	1 TNF6_RAT	P36940 rattus norv
12	171	13.3	272	1 TNF5_CHICK	Q9i8d8 gallus gall
13	160	12.4	174	1 TN15_HUMAN	Q95150 homo sapien
14	159.5	12.4	240	1 TN14_MOUSE	O43557 homo sapien
15	152.5	11.8	239	1 TN14_MOUSE	Q9gyh9 mus musculus
16	152	11.8	261	1 TNF5_BOVIN	P51749 bos taurus
17	140	10.9	261	1 TNF5_AOTTR	Q9bdm3 aotus trivi
18	140	10.9	261	1 TNF5_CALJA	Q9bdm3 callithrix
19	137.5	10.7	260	1 TNF5_MOUSE	P29548 mus musculus
20	137	10.6	261	1 TNF5_HUMAN	P29965 homo sapien
21	137	10.6	261	1 TNF5_MACMU	Q9bdm7 macaca mula
22	136.5	10.6	261	1 TNF5_RABIT	P04924 cryptolagus
23	136.5	10.6	260	1 TNF5_FELCA	Q97605 felis silve
24	134.5	10.5	260	1 TNF5_PIG	P26445 sus scrofa
25	134.5	10.5	260	1 TNF5_CANFA	Q97626 canis fami
26	132.5	10.3	234	1 TNFA_CAVPO	P51435 canis porce
27	132	10.3	261	1 TNF5_PIG	Q95mg5 sus scrofa
28	131.5	10.2	260	1 TNF5_RAT	Q92222 rattus norv
29	130	10.1	232	1 TNFA_PIG	P23583 sus scrofa
30	129.5	10.1	235	1 TNFA_PERLE	P36939 peromyscus
31	127.5	9.9	204	1 TNFB_BOVIN	Q06600 bos taurus
32	126	9.8	234	1 TNFA_HORSE	P29553 equus cabal
33	125.5	9.8	253	1 TNFA_SPAU	Q9jfg3 sparus aura

ALIGNMENTS

RESULT 1

TN10_HUMAN	STANDARD;	PRT;	281 AA.
ID	P50591;		
AC	01-OCT-1996 (Rel. 34, Created)		
DT	01-OCT-1996 (Rel. 34, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Tumor necrosis factor ligand superfamily member 10 (TNF-related apoptosis inducing ligand) (TRAIL protein) (Apo-2 ligand) (Apo-2L).		
GN	TNFSF10 OR TRAIL OR APO2L		
OS	Homo sapiens (Human)		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RI	SEQUENCE FROM N.A.		
RP	MEDLINE=96111955; PubMed=8777713;		
RX	Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P., Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A., Goodwin R.G.,		
RA	"Identification and characterization of a new member of the TNF family that induces apoptosis."		
RT	Immunity 3:673-682(1995).		
RL	SEQUENCE FROM N.A.		
RN	[2]		
RP	TISSUE=Placenta;		
RC	MEDLINE=9627864; PubMed=8663110;		
RX	Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A., Ashkenazi A.,		
RA	"Induction of apoptosis by Apo-2 ligand, a new member of the tumor necrosis factor cytokine family."		
RT	J. Biol. Chem. 271:12687-12690(1996).		
RL	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lymph;		
RX	MEDLINE=22388257; PubMed=12477932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Kleusner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D., Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A., Ashkenazi A.,		
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RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lymph;		
RX	MEDLINE=22388257; PubMed=12477932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Kleusner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D., Pitti R.M., Marsters S.A., Ruppert S., Donahue C.J., Moore A., Ashkenazi A.,		
RT	"Induction of apoptosis by Apo-2 ligand, a new member of the tumor necrosis factor cytokine family."		
RL	J. Biol. Chem. 271:12687-12690(1996).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lymph;		

[4] X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 114-281.
 MEDLINE=20017054; PubMed=10549288;
 RA Hymowitz S.G., Christinger H.W., Fuh G., Ultsch M., O'Connell M.,
 RA Kelley R.F., Ashkenazi A., de Vos A.M.,
 RT "Triggering cell death: the crystal structure of Apo2L/TRAIL in a
 RT complex with death receptor 5.";
 RL Mol. Cell 4:563-571(1999).
 [5]
 RN X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 119-281.
 RP PubMed=10542098;
 RX Mongkolsapaya J., Grimes J.M., Chen N., Xu X.-N., Stuart D.I.,
 RA Jones E.Y., Screaton G.R.,
 RA "Structure of the TRAIL-DR5 complex reveals mechanisms conferring
 RT specificity in apoptotic initiation.";
 RL Nat. Struct. Biol. 6:1048-1053(1999).
 [6]
 RN X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 114-281.
 RP MEDLINE=99413670; PubMed=10485660;
 RX Cha S.-S., Kim M.S., Choi Y.H., Sung B.J., Shin N.K., Shin H.C.,
 RA Sung Y.C., Oh B.-H.,
 RA "2.8 Å resolution crystal structure of human TRAIL, a cytokine with
 RT selective antitumor activity.";
 RL Immunity 11:253-261(1999).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and
 CC possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity
 CC may be modulated by binding to the decoy receptors
 CC TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot
 CC induce apoptosis.
 CC -1- COFACTOR: Binds 1 zinc ion and one anionic solvent molecule per
 CC trimer.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: WIDESPREAD; MOST PREDOMINANT IN SPLEEN, LUNG
 CC AND PROSTATE.
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 CC
 CC EMBL; U37518; AAC50332.1; -;
 CC EMBL; U57059; AAB01233.1; -;
 CC EMBL; BC032722; AAH32722.1; -;
 CC PDB; 1D0G; 22-OCT-99.
 CC PDB; 1D4V; 01-NOV-99.
 CC PDB; 1D2Q; 11-FEB-00.
 CC PDB; 1DG6; 26-SEP-01.
 CC Genew; HGNC:11925; TNFRSF10.
 CC MIM; 603598; -;
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.
 CC GO; GO:0005825; C:soluble fraction; TAS.
 CC GO; GO:0005402; F:receptor binding; TAS.
 CC GO; GO:0007267; P:cell-cell signaling; TAS.
 CC GO; GO:0006917; P:induction of apoptosis; TAS.
 CC GO; GO:0007165; P:signal transduction; TAS.
 CC InterPro; IPR006052; TNF family.
 CC InterPro; IPR008983; TNF-like.
 CC InterPro; IPR003636; TNF_subf.
 CC Pfam; PF00229; TNF_1.
 CC ProDom; PD002012; TNF_subf; 1.
 CC SMART; SMC0207; TNF; 1.
 CC PROSITE; PS00251; TNF_1; 1.
 CC PROSITE; PS00049; TNF_2; 1.
 CC Cytokine; Apoptosis; Transmembrane; Signal-anchor; Metal-binding;
 KW Zinc; 3D-structure.
 FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

(POTENTIAL).
 EXTRACELLULAR (POTENTIAL).
 ZINC.

FT	DOMAIN	39	281
FT	METAL	230	230
FT	STRAND	123	127
FT	TURN	130	131
FT	TURN	137	139
FT	STRAND	149	150
FT	STRAND	163	165
FT	STRAND	167	170
FT	TURN	171	172
FT	STRAND	173	176
FT	STRAND	180	193
FT	STRAND	205	213
FT	STRAND	220	228
FT	STRAND	237	250
FT	TURN	252	253
FT	STRAND	255	260
FT	HELIX	263	265
FT	STRAND	266	267
FT	TURN	270	272
FT	STRAND	274	281
SQ	SEQUENCE	281 AA;	32509 MW; DDAAAF78DAAB2F6D CRC64;

Query Match 100.0%; Score 1287; DB 1; Length 281;
 Best Local Similarity 100.0%; Pred. No. 8.3e-99;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVKMLRTSEE	60
DB	39	TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVKMLRTSEE	98
QY	61	TISTVQEKQONISPLVREGRGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR	120
DB	99	TISTVQEKQONISPLVREGRGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR	158
QY	121	SGHSFLNHLRNGELVHEKGFYIYSQTYFRFQBEIKENTKDKQKQVYIYKTSYPD	180
DB	159	SGHSFLNHLRNGELVHEKGFYIYSQTYFRFQBEIKENTKDKQKQVYIYKTSYPD	218
QY	181	PILLMKARNCSKDAEYGLYISYQGGIFELKENDRIFVSVTNEHLIDVDHEASFFGAF	240
DB	219	PILLMKARNCSKDAEYGLYISYQGGIFELKENDRIFVSVTNEHLIDVDHEASFFGAF	278
QY	241	LVG 243	
DB	279	LVG 281	

RESULT 2
 TN10_MOUSE
 ID TN10_MOUSE STANDARD; PRT; 291 AA.
 AC P50592;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 10 (TNF-related
 DE apoptosis inducing ligand) (TRAIL protein).
 GN TNFSF10 OR TRAIL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96111955; PubMed=8777713;
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
 RA Goodwin R.G.,
 RT "Identification and characterization of a new member of the TNF
 RT family that induces apoptosis.";
 RL Immunity 3:673-682(1995).
 CC -1- FUNCTION: Cytokine that binds to TNFRSF10A/TRAILR1,
 CC TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and

possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity may be modulated by binding to the decoy receptors TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot induce apoptosis.

-!- SUBUNIT: Homotrimer (By similarity).

-!- SUBCELLULAR LOCATION: Type II membrane protein (Potential).

-!- TISSUE SPECIFICITY: WIDESPREAD.

-!- SIMILARITY: Belongs to the tumor necrosis factor family.

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EMBL; U37522; AAC52345.1; -.

HSSP; P50591; 1D0G.

MGD; MG1:107414; Tnfsf10.

InterPro; IPR006052; TNF family.

InterPro; IPR008983; TNF-like.

ProDom; PD00229; TNF; 1.

ProDom; PD002012; TNF subf; 1.

SMART; SM00207; TNF; 1.

PROSITE; PS00251; TNF; 1.

PROSITE; PS00499; TNF; 2; 1.

Cytokine; Transmembrane; Signal-anchor; Apoptosis.

DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).

TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).

DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).

CARBOHYD 52 52 N-LINKED (GLCNAC...) (POTENTIAL).

SEQUENCE 291 AA; 33477 MW; 3FEACB9F07D802 CRC64;

Query Match 67.1%; Score 863; DB 1; Length 291;

Best Local Similarity 66.1%; Pred. No. 6.8e-64;

Matches 164; Conservative 32; Mismatches 46; Indels 6; Gaps 1;

QY 1 TNELKQMDKYSKGIACFLKEDSDYDNDDESMKSPQWQKQLRQLVRKMLTSEE 60

DB 43 TNEKQIQDNYKSIKGLACFKDEDFDWDSTGELNRPCLQVQRQLYQLIEVTLTFQD 102

QY 61 TISTVQEKQKISPLVRERGPQVAAHITGRGSRNTLSSPNKNEKALGRKINSWESSR 120

DB 103 TISTVPEKQLSTPLPRGGRPKVAAHITGRGSRNSALIPISKDGLQKTESWESSR 162

QY 121 SGHSFLNLHLRNGELVHKEGFIYYSQYFRFQEE-----IKENTKNDKQWQYIYK 174

DB 163 KGHSLNHLVFRNGELVIEQEGLYIYSQYFRFQEAEDASKWVKDKVTKQLVQYIYK 222

QY 175 YTSVPDPILLKMSARNSCWSDAEYGLYSYIQQGIFELKENDRIFVSVTNEHLIDMDHEA 234

DB 223 YTSVPDPVILKMSARNSCWSDAEYGLYSYIQQGLFELKKNDRIFVSVTNEHLMDLQEA 282

QY 235 SFFGAFV 242

DB 283 SFFGAFV 290

RESULT 3

TN11 RAT

ID TN11 RAT STANDARD; PRT; 318 AA.

AC Q9E5E2; Q91Z19;

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TNF) (TNF-related ligand) (OPGL) (Osteoclast differentiation factor) (ODF).

GN TNFSF11 OR RANKL OR TRANCE OR OPGL.

OS Rattus norvegicus (Rat).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

CC NCBI_TaxID=101116;

CC [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Tibial bone;

RA MEDLINE=20540945; PubMed=11092396;

RA Xu J.X., Tan J.K., Huang L., Gao X.H., Laird R., Liu D., Wysocki S., Zheng M.H.;

RT "Cloning, sequence and functional characterization of the rat homologue of receptor activator of NF-kB ligand.";

RL J. Bone Miner. Res. 15:2178-2186(2000).

RP [2]

RP SEQUENCE OF 266-318 FROM N.A.

RC STRAIN=Fischer 344;

RA MEDLINE=21662371; PubMed=11804028;

RA Ogdren P.R., Kim N., van Wesenbeeck L., Mackay C., Mason-Savas A., Safadi F.P., Popoff S.N., Lengner C., van-Hul W., Choi Y., Marks S.C. Jr.;

RA "Evidence that the rat osteopetrotic mutation toothless (tl) is not in the TNFSF11 (TRANCE, RANKL, ODF, OPGL) gene.";

RT Int. J. Dev. Biol. 45:853-859(2001).

RL -!- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to TNFRSF11A/RANK. Osteoclast differentiation and activation factor. Augments the ability of dendritic cells to stimulate naive T-cell proliferation. May be an important regulator of interactions between T cells and dendritic cells and may play a role in the regulation of the T cell-dependent immune response. May also play an important role in enhanced bone-resorption in humoral hypercalcaemia of malignancy.

CC -!- SUBUNIT: Homotrimer (By similarity).

CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By similarity).

CC -!- TISSUE SPECIFICITY: Highly expressed in thymus and bone tissues.

CC -!- PTM: The soluble form derives from the membrane form by proteolytic processing (By similarity).

CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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EMBL; AF187319; AAG17031.1; -.

EMBL; AF425669; AAL23963.1; -.

HSSP; P50591; 1D0G.

InterPro; IPR006052; TNF family.

InterPro; IPR008983; TNF-like.

InterPro; IPR003636; TNF_subf.

ProDom; PD00229; TNF; 1.

ProDom; PD002012; TNF subf; 1.

SMART; SM00207; TNF; 1.

PROSITE; PS00251; TNF; 1; FALSE_NEG.

PROSITE; PS00499; TNF; 2; 1.

Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane; Signal-anchor.

CHAIN 1 318 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 11, MEMBRANE FORM.

FT CHAIN 141 318 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 11, SOLUBLE FORM.

FT DOMAIN 1 47 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 48 68 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).

FT DOMAIN 69 318 EXTRACELLULAR (POTENTIAL).

FT SITE 140 141 CLEAVAGE (BY SIMILARITY).

FT CARBOHYD 199 199 N-LINKED (GLCNAC...) (POTENTIAL).

FT CARBOHYD 264 264 N-LINKED (GLCNAC...) (POTENTIAL).

FT CONFLICT 317 317 I -> M (IN REF. 2).

SEQUENCE 318 AA; 35370 MW; 4B87A4D706AD096F CRC64;

CC -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THYMUS AND LYMPH NODES BUT NOT IN NONLYMPHOID TISSUES AND IS ABUNDANTLY EXPRESSED IN T CELLS BUT NOT IN B CELLS. A HIGH LEVEL EXPRESSION IS ALSO SEEN IN THE TRABECULAR BONE AND LUNG.

CC -!- PTM: N-glycosylated.

CC -!- PTM: The soluble form of isoform 1 derives from the membrane form by proteolytic processing. The cleavage may be catalyzed by ADAM17. A further shorter soluble form was observed.

CC -!- DISEASE: Deficiency in TNFSF11 results in failure to form lobulo-alveolar mammary structures during pregnancy, resulting in death of newborns. Trance-deficient mice show severe osteopetrosis, with no osteoclasts, marrow spaces, or tooth eruption, and exhibit profound growth retardation at several skeletal sites, including the limbs, skull, and vertebrae and have marked chondrodysplasia, with thick irregular growth plates and a relative increase in hypertrophic chondrocytes.

CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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CC -----

CC EMBL; AF013170; AAC71061.1; -

CC EMBL; AF019048; AAB86812.1; -

CC EMBL; AF053713; AAC40113.1; -

CC EMBL; AB008426; BAA25425.1; -

CC EMBL; AB022039; BAA36970.1; -

CC EMBL; AB022036; BAA36970.1; JOINED.

CC EMBL; AB022037; BAA36970.1; JOINED.

CC EMBL; AB022038; BAA36970.1; JOINED.

CC EMBL; AB032771; BAA97257.1; -

CC EMBL; AB032772; BAA97258.1; -

CC EMBL; AB036798; BAA97259.1; -

CC PDB; 1J7Z; 28-JAN-03.

CC PDB; 1IQ4; 14-JAN-03.

CC MGI; 1100089; Tnfsf11.

CC GO; GO:0009887; P:organogenesis; IMP.

CC GO; GO:0001503; P:ossification; IMP.

CC InterPro; IPR006052; TNF family.

CC InterPro; IPR008983; TNF-like.

CC InterPro; IPR003636; TNF_subf.

CC Pfam; PF00229; TNF; 1.

CC ProDom; PD002012; TNF_subf; 1.

CC SMART; SM00207; TNF; 1.

CC PROSITE; PS00251; TNF 1; FALSE_NEG.

CC PROSITE; PS00049; TNF 2; 1.

CC Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane; Signal-anchor; 3D-structure; Alternative splicing.

CC CHAIN 1 316 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 11, MEMBRANE FORM.

CC CHAIN 139 316 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 11, SOLUBLE FORM.

CC DOMAIN 1 48 CYTOPLASMIC (POTENTIAL).

CC TRANSMEM 49 69 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).

CC DOMAIN 70 316 EXTRACELLULAR (POTENTIAL).

CC SITE 138 139 CLEAVAGE.

CC CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).

CC VARSPIC 1 117 Missing (in isoform 3).

CC VARSPIC 14 44 (FTId=VSP_006448).

CC SSEMSPGVPEHGLHAPSAPAPAPPA -> TP (in isoform 2).

CC (FTId=VSP_006449).

CC G -> D (IN REF. 2).

CC MISSING (IN REF. 5).

CC CONFLICT 99 99

CC CONFLICT 141 143

CC STRAND 164 169

CC TURN 171 172

CC STRAND 181 182

FT STRAND 186 187

FT TURN 191 192

FT STRAND 194 196

FT STRAND 198 201

FT TURN 202 203

FT STRAND 204 207

FT STRAND 211 224

FT HELIX 225 227

FT STRAND 234 245

Query Match 18.5%; Score 238.5; DB 1; Length 316;

Best Local Similarity 27.4%; Pred. No. 1.9e-12;

Matches 71; Conservative 44; Mismatches 95; Indels 49; Gaps 9;

Qy 9 DKYSKSGIACF-----LKEDDSYWDP--NDEESMSPCMQVKQLQVLEKMLRTSEET 61

Db 78 NRISDSTHCFYRILRLHENAGLQDSTLESDTLPSCRMKQAFQAVQK----- 128

Qy 62 ISTVQEQKNISPL-----VREGPQVRA--AHITGRGSNTLSGPNK 104

Db 129 -----ELQHIVGQRFSGAPAMMEGSLDVAQRKPEAQPFALHT-----INAASIPSGS 178

Qy 105 NEKALGRKINSWSSRGHSFLNLHLNGELVIHEKGFYIYSQIYVERFQEBIKENTKN 164

Db 179 HKVTL-----SSVYHDR--GWAKISNMTLSNGKLRVQDGFYLYANICFRHHETSGSVPTD 233

Qy 165 DKQWQYIYKYT--SYDPILLKMSARNSCWSKDAEYGLYSIYQGIFELKENDRIFVSVT 223

Db 234 YLQLMVVTVKTSIKIPSSHNLKMGSTKQWNSGSEPHFYINVGPFKLAGEISIQVS 293

Qy 224 NEHLIDMDHEASFGAFLV 242

Db 294 NPSLLDPDQDATVFGAFKV 312

RESULT 5

TN11_HUMAN

ID TN11_HUMAN STANDARD; PRT; 317 AA.

AC O14788; O14723; Q96Q17; Q9P2Q3;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor ligand superfamily member 11 (Receptor activator of nuclear factor kappa B ligand) (RANKL) (TNF-related activation-induced cytokine) (TRANCE) (Osteoprotegerin ligand) (OPGL) (Osteoclast differentiation factor) (ODF).

DE Differentiation factor (ODF).

GN TNFSF11 OR RANKL OR TRANCE OR OPGL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]_TaxID=9606;

SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Bone marrow, and Peripheral blood;

RX MEDLINE=98032977; PubMed=9367155;

RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C., Tonetsko M.E., Roux E.R., Teepe M.C., DuBoise R.F., Cosman D., Galibert L.

RA "A homologue of the TNF receptor and its ligand enhance T-cell growth and dendritic-cell function."

RL Nature 390:175-179(1997).

RN [2]

SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Lymph node;

RX MEDLINE=98227661; PubMed=9568710;

RA Lacey D.L., Timms E., Tan H.-L., Kelley M.J., Dunstan C.R., Hsu H., Burgess T., Elliott R., Colombero A., Elliott G., Scully S., Hsu H., Sullivan J., Hawkins N., Davy E., Capparelli C., Eli A., Qian Y.-X., Kaufman S., Sarosi I., Shalhoub V., Senaldi G., Guo J., Delaney J., Boyle W.J.

RA "Osteoprotegerin ligand is a cytokine that regulates osteoclast differentiation and activation."

RT Cell 93:165-176(1998).

[3]
 RN SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RA Ikeda T., Kuroyama H., Hirokawa K.;
 RT "Determination of human RANKL isoforms."
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 [4]
 RN SEQUENCE OF 73-317 FROM N.A.
 RC TISSUE=Thymocytes;
 RX MEDLINE=97460112; PubMed=9312132;
 RA Wong B.R., Rho J., Arron J., Robinson E., Orlicki J., Chao M.,
 RA Kalachikov S., Cayani E., Bartlett P.S. III, Frankel W.N., Lee S.Y.,
 RA Choi Y.;
 RT "RANK is a novel ligand of the tumor necrosis factor receptor family
 RT that activates C-Jun N-terminal kinase in T cells";
 RL J. Biol. Chem. 272:25190-25194(1997).
 [5]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Tongue;
 RX MEDLINE=20175237; PubMed=10708588;
 RA Nagai M., Kyakumoto S., Sato N.;
 RT "Cancer cells responsible for humoral hypercalcemia express mRNA
 RT encoding a secreted form of ODF/TRANCE that induces osteoclast
 RT formation.";
 RL Biochem. Biophys. Res. Commun. 269:532-536(2000).
 CC -I- FUNCTION: Cytokine that binds to TNFRSF11B/OPG and to
 CC TNFRSF11A/RANK. Osteoclast differentiation and activation factor.
 CC Augments the ability of dendritic cells to stimulate naive T-cell
 CC proliferation. May be an important regulator of interactions
 CC between T cells and dendritic cells and may play a role in the
 CC regulation of the T cell-dependent immune response. May also play
 CC an important role in enhanced bone-resorption in humoral
 CC hypercalcemia of malignancy.
 CC -I- SUBUNIT: Homotrimer (By similarity).
 CC -I- SUBCELLULAR LOCATION: Type II membrane protein (isoforms 1 and 3);
 CC Secreted (isoform 2). A soluble form of isoform 1 arises by
 CC proteolytic processing (By similarity).
 CC -I- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=3;
 CC Name=1;
 CC IsoId=O14788-1; Sequence=Displayed;
 CC Name=2; Synonyms=SODF;
 CC IsoId=O14788-2; Sequence=VSP_006447;
 CC Name=3;
 CC IsoId=O14788-3; Sequence=VSP_006446;
 CC -I- TISSUE SPECIFICITY: HIGHEST IN THE PERIPHERAL LYMPH NODES BUT WEAK
 CC IN SPLEEN, PERIPHERAL BLOOD LEUCOCYTES, BONE MARROW, HEART,
 CC PLACENTA, SKELETAL MUSCLE, STOMACH AND THYROID.
 CC -I- INDUCTION: UPREGULATED BY T CELL RECEPTOR STIMULATION.
 CC -I- PTM: The soluble form of isoform 1 derives from the membrane form
 CC by proteolytic processing (By similarity). The cleavage may be
 CC catalyzed by ADAM17.
 CC -I- SIMILARITY: Belongs to the tumor necrosis factor family.

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 DR EMBL; AF019047; AAB86811.1; -
 DR EMBL; AF053712; AAC39731.1; -
 DR EMBL; AB064269; BAB79694.1; -
 DR EMBL; AB061227; BAB71768.1; -
 DR EMBL; AB064270; BAB79695.1; -
 DR EMBL; AF013171; AAC51762.1; -
 DR EMBL; AB037599; BAA90488.1; -
 DR HSSP; P50591; 1D0G.
 DR Genew; HGNC:11926; TNFSF11.
 DR MIM; 602642; -
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0005887; C:integral to plasma membrane; NAS.

DR GO; GO:0005164; F:tumor necrosis factor receptor binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR GO; GO:0030316; P:osteoclast differentiation; NAS.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF-like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF 1; FALSE_NEG.
 DR PROSITE; PS0049; TNF 2; 1.
 KW Cytokine; Differentiation; Receptor; Glycoprotein; Transmembrane;
 KW Signal-anchor; Alternative splicing.
 FT CHAIN 1 317
 FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT MEMBER 11. MEMBRANE FORM.
 FT TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT MEMBER 11. SOLUBLE FORM (BY SIMILARITY).
 FT CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT CLEAVAGE (BY SIMILARITY).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT Missing (in isoform 3).
 FT /FTid=VSP_006446.
 FT VARSPLTC 1 47
 FT Missing (in isoform 2).
 FT /FTid=VSP_006447.
 FT CONFLICT 194 194 A -> G (IN REF. 4).
 FT SEQUENCE 317 AA; 35478 MW; 76617646348097F CRC64;
 Query Match 18.3%; Score 235.5; DB 1; Length 317;
 Best Local Similarity 25.3%; Pred. No. 3.3e-12;
 Matches 65; Conservative 51; Mismatches 98; Indels 43; Gaps 9;
 QY 9 DKYKSGIACF-----LKED-----DSYWDNDDESMNSPCWQVKW-----OLQOLVR 51
 DB 77 NRISGDGHCIYRILRLHENDADFOPTLESQDTKLIPDSCKRIKQAFQGVQKELQHV 136
 QY 52 KMILRTSEETI-----STVQEQKQNI SPLVREGRQFVAHHITGRGNTLSPPSKNE 106
 DB 137 SQHIRAEKAMVDGSLDLAKRSKLEAQP-----AHLT-----INATDIPSGSHK 181
 QY 107 KALGKINSWSSRSRSGHSPFLSNLHRLNGELVIHEKGFYIYQTYRFRFOEIKENTKNDK 166
 DB 182 VSL-----SSWYHDR-GWAKISNMTFTSGKLIVNQDGFYLYANICFRHHETSGDLATEYL 236
 QY 167 QMWQVIYKYT-SYDPDILLMKSAENSQSKDAEYGLYSIYQGGIFELKENDRIFVSVTNE 225
 DB 237 QLMVYVTKTSIKIPSSHTLMKGGSTKYWSGNSSEFHYISINVGGFFKLRSGEISIEVSNP 296
 QY 226 HLIDNDHEASFPGLV 242
 DB 297 SLDDPDQDATYFGAFKV 313
 RESULT 6
 TNF6_MOUSE
 ID TNF6_MOUSE STANDARD; PRT; 279 AA.
 AC P41047; Q61217; Q9RUF2;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
 DE ligand).
 GN TNFSF6 OR FASL OR APT1L1 OR GLD.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM FASL).
 RX MEDLINE=94185175; PubMed=7511063;

QY 165 DKOMQVYIY-KYTSYDPDILLMKASR-NSCWSKDAEYGLYSIYQGGIFELKENDRIFSV 222
 DB 202 NQPLAHKVMRSKYPEDVLMEERLNYCTT--GQIWAHSSYLGAVENTASADHLYVNI 259
 QY 223 TNEHLIDMDHEASFFGAF 240
 DB 260 SQLSLINFESKTFGLY 277

RESULT 7
 TNF6_CERTO STANDARD; PRT; 280 AA.
 AC Q9BDJ1.
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
 DE (CD95L protein).
 GN TNFSF6 OR FASL OR CD95L.
 OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecidae.
 OX NCBI_TaxID=9531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 CC -!- FUNCTION: Cytokine that binds to TNFSF6/FAS, a receptor that
 CC transduces the apoptotic signal into cells. May be involved in
 CC cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFSF6/FAS-mediated apoptosis may have a role in the induction of
 CC peripheral tolerance, in the antigen-stimulated suicide of mature
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
 CC modulates its effects (By similarity).
 CC -!- SUBUNIT: Homotrimer (Probable).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
 CC similarity).
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF34847; AK37606.1; -.
 DR HSPSP, P01375; 4TSV.
 DR InterPro; IPR008064; Fas_ligand.
 DR InterPro; IPR006053; TNF_abc.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; P01681; FASLIGAND.
 DR PRINTS; P01234; TNFECROSISFCT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF 1; 1.
 DR PROSITE; PS0049; TNF 2; 1.
 KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor.
 FT CHAIN 1 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT MEMBER 6, MEMBRANE FORM.
 FT CHAIN 129 280 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY

FT DOMAIN 1 80 MEMBER 6, SOLUBLE FORM (BY SIMILARITY).
 FT TRANSMEM 81 101 CYTOPLASMIC (POTENTIAL).
 FT SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT PRO-RICH.
 FT PRO-PRO.
 FT POLY-PRO.
 FT CLEAVAGE (BY SIMILARITY).
 FT POTENTIAL.
 FT DISULFID 201 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 249 249 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 280 AA; 31407 MW; 729EA60067B7D398 CRC64;
 Query Match 14.4%; Score 185.5; DB 1; Length 280;
 Best Local Similarity 27.4%; Pred. No. 3.7e-08;
 Matches 55; Conservative 42; Mismatches 77; Indels 27; Gaps 8;
 QY 44 WQLRQLVRKMI-LR--TSEETISTVQEKQONISPLVRERGPQVAAHITGTRGRSNTLS 100
 DB 101 FQLFHLQKELAELESTSQKHTASSLEKQIGHSPPEKKEQKVAHLTG-----K 151
 QY 101 PMSKNEKALGRKINSWESSRSGHSFLNLHLRNGELVIEHKGFYIYSQTYFRFOBEIKE 160
 DB 152 PMSRSMPL-----EWEDT-YGIVLLSGVKYKGGVIVNETGLYFYVKYVFRGQ----- 199
 QY 161 NTXNDKQMVYIY-KYTSYDPDILLMKASRNSCWSKDAEYGLYSIYQGGIFELKENDRIF 219
 DB 200 -SCTNLEPLSHKVMRSKYPQDLVMEGRKMS-YCTTGQWMAHSSYLGAVENTSTHLY 257
 QY 220 VSVTNEHLIDMDHEASFFGAF 240
 DB 258 VNVSELSLVNFESQTFFGLY 278

RESULT 8
 TNF6_MACMU STANDARD; PRT; 280 AA.
 AC Q9MYL6; Q9BDM5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen ligand)
 DE (CD95L protein).
 GN TNFSF6 OR FASL OR CD95L.
 OS Macaca mulatta (Rhesus macaque),
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
 OS Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Cercopithecidae.
 OX NCBI_TaxID=9544, 9541, 9545;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphocytes;
 RX MEDLINE=21383618; PubMed=11491535;
 RA Villinger F., Bostik P., Wayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 RT Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 CC
 CC SEQUENCE FROM N.A.
 RC SPECIES=M. mulatta, M. fascicularis, and M. nemestrina;
 RA Kirii Y., Inoue T., Yoshino K.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
 CC transduces the apoptotic signal into cells. May be involved in
 CC cytotoxic T cell mediated apoptosis and in T cell development.
 CC TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
 CC peripheral tolerance, in the antigen-stimulated suicide of mature
 CC T cells, or both. Binding to the decoy receptor TNFRSF6B/DcR3
 CC modulates its effects (By similarity).


```

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [8]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Blood;
RA Matsumura M., Nakanishi Y., Ohba Y.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
RN [9]
RP CHARACTERIZATION, AND MUTAGENESIS OF PRO-206; TYR-218 AND PHE-275.
RX MEDLINE=97373583; PubMed=9228059;
RA Schneider P., Bodmer J.-L., Holler N., Mattmann C., Scuderi P.,
RA Tersikh A., Peitsch M.C., Rechoff J.;
RT "Characterization of Fas (Apo-1, CD95)-Fas ligand interaction.";
RL J. Biol. Chem. 272:18827-18833(1997).
RN [10]
RP PROCESSING.
RX MEDLINE=98087475; PubMed=9427603;
RA Tanaka M., Itai T., Adachi M., Nagata S.;
RT "Downregulation of Fas ligand by shedding.";
RL Nat. Med. 4:31-36(1998)
CC -1- FUNCTION: Cytokine that binds to TNFRSF6/FAS, a receptor that
transduces the apoptotic signal into cells. May be involved in
cytotoxic T cell mediated apoptosis and in T cell development.
TNFRSF6/FAS-mediated apoptosis may have a role in the induction of
peripheral tolerance, in the antigen-stimulated suicide of mature
T cells, or both. Binding to the decoy receptor TNFRSF6B/DCR3
modulates its effects.
CC -1- SUBUNIT: Homotrimer (Probable).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. May be released
into the extracellular fluid, probably by cleavage form the cell
surface.
CC -1- ALTERNATIVE PRODUCTS:
Name=1; Event=Alternative splicing; Named isoforms=2;
Name=2; IsoId=PA48023-1; Sequence=Displayed;
Name=3; IsoId=PA48023-2; Sequence=VSP_006443, VSP_006444;
CC -1- PTM: N-glycosylated.
CC -1- PTM: The soluble form derives from the membrane form by
proteolytic processing.
CC -1- DISEASE: Defects in TNFRSF6 are a cause of autoimmune
lymphoproliferative syndrome (ALPS) [MIM:601859]; also known as
Canale-Smith syndrome (CSS). ALPS is a childhood syndrome
involving hemolytic anemia and thrombocytopenia with massive
lymphadenopathy and splenomegaly.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -1- DATABASE: NAME=PRO; NOTE=PRO 2:59-69(2001);
WWW="http://www.ncbi.nlm.nih.gov/prov/guide/333879674_g.htm".
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; X89102; CAA61474.1; -
DR EMBL; U08137; AAC50071.1; -
DR EMBL; U11821; AAC50124.1; -
DR EMBL; D38122; BAA07320.1; -
DR EMBL; AF288573; AAG60017.1; -
DR EMBL; Z96050; CAB09424.1; -
DR EMBL; BC017502; AAH17502.1; -
DR EMBL; AB013303; BAA32542.1; -
DR PIR; I38707; I38707.
DR HSSP; P01375; 1TNF.
DR Genew; HGNC:11936; TNFSF6.
DR MIM; 134638; -
DR MIM; 601859; -
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0005102; P:receptor binding; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.
DR GO; GO:0006917; P:induction of apoptosis; TAS.
GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRODom; PD002012; TNF_subf; 1.
DR SMART; SMC0207; TNF; 1.
DR PROSITE; PS00251; TNF; 1; 1.
DR PROSITE; PS00449; TNF; 2; 1.
KW Cytokine; Apoptosis; Transmembrane; Glycoprotein; Signal-anchor;
KW Alternative splicing; Antigen.
FT CHAIN 1 281
FT CHAIN 130 281
FT DOMAIN 1 80
FT TRANSMEM 81 102
FT DOMAIN 103 281
FT DOMAIN 4 70
FT DOMAIN 45 65
FT SITE 129 130
FT DISULFID 202 233
FT CARBOHYD 184 184
FT CARBOHYD 250 250
FT CARBOHYD 260 260
FT VARSPPLIC 117 127
FT FTId=VSP_006443.
FT VARSPPLIC 128 281 Missing (in isoform 2).
FT FTId=VSP_006444.
FT MUTAGEN 206 206 P->D,F,R: LOWERS BINDING TO TNFRSF6 AND
FT MUTAGEN 218 218 REDUCES CYTOTOXICITY MORE THAN 100-FOLD.
FT MUTAGEN 275 275 Y->F,R: LOWERS BINDING TO TNFRSF6 AND
CYTOTOXICITY.
FT SEQUENCE 281 AA; 31485 MW; A8A6EB358246E9BB CRC64;
Query Match 14.2%; Score 182.5; DB 1; Length 281;
Best Local Similarity 27.4%; Pred. No. 6.6e-08;
Matches 57; Conservative 40; Mismatches 70; Indels 41; Gaps 10;
QY 44 WQLRQLVKKMI-LRTSEETISTVQEKQONI---SPLVREGRQPVAAHITCTGRSNTLS 99
DB 102 FQLFHLQELAELESTQMTASLEKQIGHSP-PPEKKELKVAHLT---GKSNSRS 157
QY 100 SPNKNEXALGRKINSMESSRSGHSFLSNLHRLNGELVHKGPIYYSQTYFRQBEIK 159
DB 158 MP-----LEWEDT-YGIVLLSGVKYKKGGLVINETGLYFVYSKYVFRGQ---- 200
QY 160 ENTQNDKQWQVIY-KYTSYDPDILLMKSAKNS-----CWSKDAEYGLYSYGGIFEL 212
DB 201 --SCNNFLSHKVMNRNSKYPQDLVMEGQWMSYCTTQGMAR-----SSYLGAENVL 251
QY 213 KENDRIFVSVTNEHLIDMDHEASPFQAF 240
DB 252 TSADHLVNVSELSLVNFEESQTFFGLY 279
RESULT 10
TNF6_PIG
ID TNF6_PIG STANDARD; PRT; 282 AA.
AC Q9BEA8; Q95M04; Q95N10;
DC 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 6 (FAS antigen
ligand).

```


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OM protein - protein search, using sw model

Run on: June 3, 2004, 08:53:00 ; Search time 20 Seconds

(without alignments)

1168.727 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281

Perfect score: 1287

Sequence: 1 TNELKQMDKYTSKSGIACFL.....NEHLIDMDHEASFFGAFVVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_78.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	189.5	14.7	279	2 A53062	Fas ligand - mouse
2	182.5	14.2	281	2 I38707	Fas ligand - human
3	177.5	13.8	278	2 A49266	Fas ligand - rat
4	152	11.8	261	2 S32090	CD40 ligand - bovi
5	138.5	10.8	260	2 S21738	CD40 ligand - mous
6	137	10.6	261	2 I3476	CD40 ligand - huma
7	134.5	10.5	204	1 S17289	tumor necrosis fac
8	131.5	10.2	234	1 A25451	tumor necrosis fac
9	130	10.1	232	1 S12606	tumor necrosis fac
10	129.5	10.1	235	1 S2460	tumor necrosis fac
11	127.5	9.9	204	1 S24641	lymphotoxin - bovi
12	126	9.8	234	1 J01344	tumor necrosis fac
13	123	9.6	233	1 QHUN	tumor necrosis fac
14	122	9.5	205	1 QHUX	lymphotoxin alpha
15	121	9.4	235	1 QHUN	tumor necrosis fac
16	121	9.4	235	1 QHUN	tumor necrosis fac
17	120	9.3	233	1 S22052	tumor necrosis fac
18	117.5	9.1	234	1 JH0529	tumor necrosis fac
19	115.5	9.0	193	2 S06192	tumor necrosis fac
20	114	8.9	202	1 B27303	tumor necrosis fac
21	113.5	8.8	185	2 S2715	tumor necrosis fac
22	113	8.7	233	1 S24642	tumor necrosis fac
23	111.5	8.7	202	1 JH0869	tumor necrosis fac
24	108.5	8.4	306	2 I49139	tumor necrosis fac
25	107	8.3	197	1 JH0309	lymphotoxin-beta
26	105	8.2	638	1 QH02M	tumor necrosis fac
27	102.5	8.0	652	1 I48083	mRNA maturase b14
28	102	7.9	244	2 A46066	amphotropic murine
29	98.5	7.7	233	2 S1686	lymphotoxin beta - tumor necrosis fac

RESULT 1

A53062

Fas ligand - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C:Accession: A53062

R:Takahashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Cell 76, 969-976, 1994

A:Title: Generalized lymphoproliferative disease in mice, caused by a point mutation

A:Reference number: A53062; MUID:94181175; PMID:7511083

A:Accession: A53062

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-279 <TAK>

A:Cross-references: GB:U06948; NID:G473564; PIDN:AAA17800.1; PID:G473565

Query Match

Best Local Similarity 14.7%; Score 189.5; DB 2; Length 279;

Matches 51; Conservative 50; Mismatches 64; Indels 33; Gaps 9;

QY 45 QLRQVRKXVILRTSEETISTYQEKQNIISPLVREGRQVAAHITGRGRSNTLSSPNSK 104
DB 111 ELREFTNQSL-----KVSSPEKQIANPSTPSEKKEPRSV-AHLTG-----NPHSR 154
QY 105 NEKALGRKINSWSSRSRSHSLNLHRLNSELVHEKGFYIYSQTYPRQERIKENTKN 164
DB 155 SIPL-----EWEDT-YGTALISGVKYKGLVINETGLYFVYSKYVFRGQ-----SCN 201
QY 165 DKQWQVYIY-KYTSYPPFILMKSR-NSCWSKDAEYGLYSITYQGGIFELKENDRIEVS 222
DB 202 NOPLNHKVMYNSKYPEDLVLMEEKRLNYCTT--GQIWAHSSYLGA VFNLTSDHLYVNI 259
QY 223 TNEHLIDMDHEASFFGAF 240
DB 260 SLSLINFEEKTFPGLY 277

RESULT 2

I38707

Fas ligand - human

C:Species: Homo sapiens (man)

C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C:Accession: I38707; J02340; S57565; I38554

R:Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.

Int. Immunol. 6, 1567-1574, 1994

A:Title: Human Fas ligand: gene structure, chromosomal location and species specific

A:Reference number: I38707; MUID:95127560; PMID:7826947

A:Accession: I38707

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-281 <RES>

A:Cross-references: EMBL:U11821; NID:G595430; PIDN:AAC50124.1; PID:G595431

protein kinase, pr
hypothetical prote
chromodomain hali
heat shock transcr
cardiac muscle fac
probable membrane
DNA ligase homolog
hypothetical prote
myosin-light-chain
NBS-LRR type resis
alpha-N-arabinofur
FAB1 protein - yea
DNA-directed DNA p
protein C4788.8 [i
hypothetical prote
mitogen-activated

ALIGNMENTS

R;Mita, E.; Hayaishi, N.; Iio, S.; Takehara, T.; Hijioka, T.; Kasahara, A.; Fusamoto, H.; Biochem. Biophys. Res. Commun. 204, 468-474, 1994
A;Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.
A;Reference number: JC2340; MUID:95071350; PMID:7980502
A;Accession: JC2340
A;Molecule type: DNA
A;Residues: 1-281 <MT>
A;Cross-references: GB:D38122; DDBJ:D29820; NID:G601892; PID:BA07320.1; PID:gl369902
R;Schatzlein, C.E.
A;Reference number: S57565
A;Accession: S57565
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-281 <SCH>
A;Cross-references: EMBL:X89102; NID:G687455; PID:G687456
R;Aderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; G. J. Exp. Med. 181, 71-77, 1995
A;Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.
A;Reference number: I38554; MUID:95105731; PMID:7528780
A;Accession: I38554
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-281 <RE2>
A;Cross-references: EMBL:U08137; NID:G624627; PID:AA050071.1; PID:G624628
C;Genetics:
A;Gene: FasL
A;Introns: 151/1; 116/3
A;Keywords: glycoprotein; transmembrane protein
F;80-102/Domain: transmembrane #status predicted <TM>
F;76,184,250/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 14.2%; Score 182.5; DB 2; Length 281;
Best Local Similarity 27.4%; Pred. No. 4.4e-08;
Matches 57; Conservative 40; Mismatches 70; Indels 41; Gaps 10;
Qy 44 WQLQQLVRLTSTETISVQEKQNI---SPLVRERGQPVAAHITGTRGRNTLS 99
Db 102 FQLFLKELAELESTSQMTASLEKQGHPSF-PPEKLEKLVAAHITGTRGRNTLS 157
Qy 100 SPNSKNEKALGRKINSWESSRSHSFLSNLHRLNGELVIEHKGFFYYISQTYFRFQEI 159
Db 158 MP-----LEWEDT-YGIVLLSGVYKKGGLVNETGLYFYVSKYFRGQ--- 200
Qy 160 ENTNRDKQMVYI-KYTSYDPDILLMKARS-----CWSDAEVGLSYIYOGGIFEL 212
Db 201 --SCNNPLSHKVMYNSKYPQDLVMEGKMSYCTTGQWMA-----SSYLGA VFN 251
Qy 213 KENDRIFYVSVTNEHLIDMDHEASFGAF 240
Db 252 TSADHLVNVSELSLVNFEESQTFGLY 279
RESULT 3
A49266
fas ligand - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
R;Accession: A49266
R;Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A;Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor gene family.
A;Reference number: A49266; MUID:94084792; PMID:7505205
A;Accession: A49266
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-278 <SD>
A;Cross-references: GB:U03470; NID:G440178; PID:AA052129.1; PID:G440179
C;Keywords: glycoprotein; transmembrane protein
Query Match 13.8%; Score 177.5; DB 2; Length 278;
Best Local Similarity 27.5%; Pred. No. 1.2e-07;
Matches 50; Conservative 39; Mismatches 64; Indels 29; Gaps 8;

Qy 62 ISTVQEKQNIISPLVRERGQPVAAHITGTRGRNTLSLSPNSKNEKALGRKINSWESSR 120
Db 121 VSSFEKQIANSTPSETKQPSV-AHLTGNPRSSIFL-----EWEDT- 162
Qy 121 SGHSFLSNLHRLNGELVIEHKGFFYYISQTYFRFQEI KENTKNDKQMVYI-KYTSY 179
Db 163 YGTALISGVYKKGGLVINEAGLYFYVSKYFRGQ-----SCNSQPLSHKVMYRNF 216
Qy 180 DPILLMKAR-NSCWSDAEVGLSYIYOGGIFELKENDRIYFVSVTNEHLIDMDHEASFG 238
Db 217 GDLVLMEEKLNYCTT--GQIWAHSSYLGA VFNLTADHLVYVNTSLSLINFESKTF 274
Qy 239 AF 240
Db 275 LY 276
RESULT 4
S53090
CD40 ligand - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
R;Accession: S53090
R;Mertens, B.E.L.C.; Muriuki, M.
A;Description: Cloning of bovine CD40L and homology to bovine TNFA and TNFB.
A;Reference number: S53090
A;Accession: S53090
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-261 <MER>
A;Cross-references: EMBL:Z48469; NID:G732569; PID:CAA88363.1; PID:G732570
Query Match 11.8%; Score 152; DB 2; Length 261;
Best Local Similarity 27.1%; Pred. No. 1.6e-05;
Matches 55; Conservative 39; Mismatches 77; Indels 32; Gaps 10;
Qy 39 CWQVQQLRQLVRKMLRTSETISVQEKQNIISPLVRERGQPVAAHITGTRGRNTLS 98
Db 84 CEIEISRFEDLV-KDQMNKE-----VKKKEKNFEMHKGQDQFP-IAAHV----- 127
Qy 99 SSPNSKNEKALGRKINSWESSRSHSFLSN--LHLRNG-ELVIEHKGFFYYISQTYFRFQ 155
Db 128 SPASKTTSVL-----QW--APKGYTSLNVLNLTLENGKQLAVKEQGYIYIYQVTFCSN 180
Qy 156 EBIKENTKNDKQMVYIYKYTSYDPDILLMKARSNSCWSDAEVGLSYIYOGGIFELKEN 215
Db 181 RE-----TLQAPPIASLCLKSPSGSERILLRAANTHSSSKPC--QQQSHLGGVFELOSG 234
Qy 216 DRIFVSVTNEHLIDMDHEASFG 238
Db 235 ASVFNVTDPQSVSHGTGFTSFG 257
RESULT 5
S21738
CD40 ligand - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 05-Nov-1999
R;Accession: S21738
R;Armitage, R.J.; Fanslow, W.C.; Strockbine, L.; Sato, T.A.; Macduff, J.; Cosman, D.; Spriggs, M.K.
Nature 357, 80-82, 1992
A;Title: Molecular and biological characterization of a murine ligand for CD40.
A;Reference number: S21738; MUID:92244364; PMID:1374165
A;Accession: S21738
A;Molecule type: mRNA
A;Residues: 1-260 <ARM>
A;Cross-references: EMBL:X65453; NID:G50351; PID:CAA46448.1; PID:G50352
C;Keywords: glycoprotein; transmembrane protein
F;23-46/Domain: transmembrane #status predicted <TM>
F;47-260/Domain: extracellular #status predicted <EXT>

F:239/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.8%; Score 138.5; DB 2; Length 260;
Best Local Similarity 25.1%; Pred. No. 0.00023;
Matches 47; Conservative 37; Mismatches 72; Indels 31; Gaps 8;
QY 39 CQVQKWLRLQVRKMLRTSBEETISTVQEKQOONISPLVRERGQORVAAHITGTRGRSNTL 98
DB 84 CEEERQEDLVKQITLTK-----EEKENSFENQRGDEDPQIAAHV-----V 126
QY 99 SSPNSKNEKALGRKINSWESSRSHSFLSNL-HLRNG-ELVHEKGFYIYSQTYFRFOE 156
DB 127 SEANSNAASVL-----QW-AKGGYTTMKNLVLNLENGKQLTVKREGLYVYVTVQVFCNSR 180
QY 157 EIKENTKDKQWQVYKYTSYPPDILLMKSRNSCWSDAEVGLXSIYOGGIFELKEND 216
DB 181 E-----PSSQRFIVGLWLKPIGSEIRILLAAANTHSSQLCEQ--QSVHLGGVFELOQA 234
QY 217 RIFVSVT 223
DB 235 SVFVNVT 241

RESULT 6

CD40 ligand - human
N:Alternate names: glycoprotein 39; hCD40-L protein; T-cell antigen gp39; TRAP protein
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence revision 02-Jul-1996 #text change 20-Apr-2001
C:Accession: S28017; JH0793; S26694; S28852; I53476; S25584; S30593
R:Hollenbaugh, D.; Grosmaire, L.S.; Kullas, C.D.; Chalupny, N.J.; Braesch-Andersen, S.; EMBO J. 11, 4313-4321, 1992
A:Title: The human T cell antigen gp39, a member of the TNF gene family, is a ligand for CD40
A:Reference number: S28017; MUID:93049181; PMID:11385114
A:Accession: S28017
A:Molecule type: mRNA
A:Residues: 1-261 <HOI>
A:Cross-references: EMBL:Z15017; NID:G38483; PIDN:CAA78737.1; PID:G38484
R:Spriggs, M.K.; Amitage, R.J.; Strockbine, L.; Clifford, K.N.; Macduff, B.M.; Sato, T. J. Exp. Med. 176, 1543-1550, 1992
A:Title: Recombinant human CD40 ligand stimulates B cell proliferation and immunoglobulin synthesis
A:Reference number: JH0793; MUID:93094757; PMID:1281209
A:Accession: JH0793
A:Molecule type: mRNA
A:Residues: 1-261 <SPR>
A:Cross-references: GB:K67878; NID:G38411; PIDN:CAA48077.1; PID:G38412
R:Graf, D.; Korthauer, U.; Mages, H.W.; Senger, G.; Kroczeck, R.A. Eur. J. Immunol. 22, 3191-3194, 1992
A:Title: Cloning of TRAP, a ligand for CD40 on human T cells.
A:Reference number: S26694; MUID:93078854; PMID:1280226
A:Accession: S26694
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-261 <GRA>
A:Cross-references: EMBL:X68550; NID:G37269; PIDN:CAA48554.1; PID:G37270
R:Gauchat, J.F.; Aubry, J.P.; Mazzei, G.; Life, P.; Jomotte, T.; Elson, G.; Bonnefoy, J. P. J. Immunol. 155, 259-266, 1995
A:Title: Human CD40-ligand: molecular cloning, cellular distribution and regulation of expression
A:Reference number: S28852; MUID:93138085; PMID:7678552
A:Accession: S28852
A:Molecule type: mRNA
A:Residues: 1-261 <GAU>
A:Cross-references: EMBL:L07414; NID:G180123; PIDN:AAA35662.1; PID:G180124
A:Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 6-Gln
C:Genetics:
A:Gene: GDB:CD40LG; HUGM1; IND3
A:Cross-references: GDB:120632; OMIM:308230
A:Map position: Xq26-Xq26
C:Keywords: Glycoprotein; transmembrane protein
F:13-44/Domain: transmembrane #status predicted <TMM>
F:45-261/Domain: extracellular #status predicted <EXT>
F:6,240/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.6%; Score 137; DB 2; Length 261;
Best Local Similarity 24.6%; Pred. No. 0.00031;
Matches 52; Conservative 38; Mismatches 73; Indels 48; Gaps 11;
QY 39 CQVQKWLRLQVRKMLRTSBEETISTVQEKQOONISPLVRERGQORVAAHITGTRGRSNTL 98
DB 84 CEEIKSQFEGVDIML-NKEET-----KENSFENQKGDQNPQ-IAAHV-----I 127
QY 99 SSPNSKNEKALGRKINSWESSRSHSFLSNL-HLRNG-ELVHEKGFYIYSQTYFRFOE 155
DB 128 SEASSTKTVL-----QW--AERGYTTMKNLVLNLENGKQLTVKROGLYIYIAQVTFCSN 180
QY 156 EIKENT-----KNDKQWQVYKYTSYPPDILLMKSRNSCWSDAEVGLXSIYOGG 207
DB 181 REASSQAPFFASLCLKSPGRFER-----ILLRAANTHSSAKPC--GQSQIHLG 226
QY 208 GIFELKENDRIFSVYTNHEHLIDMDHEASFFG 238
DB 227 GVPELOPGASGVFNVTDPQSQVSHGTGTFSGF 257

RESULT 7

SL7289
tumor necrosis factor beta precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999
C:Accession: S17289
R:Kuhnert, P.; Wuehrlich, C.; Peterhans, E.; Pauli, U. Gene 102, 171-178, 1991
A:Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative analysis
A:Reference number: S17289; MUID:91340150; PMID:1874444
A:Accession: S17289
A:Molecule type: DNA
A:Residues: 1-204 <KUH>
A:Cross-references: EMBL:X54859; NID:G2132; PIDN:CAA38638.1; PID:G2133
C:Genetics:
A:Introns: 32/3; 68/1
A:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-204/Product: tumor necrosis factor beta #status predicted <MAT>

Query Match 10.5%; Score 134.5; DB 1; Length 204;
Best Local Similarity 24.7%; Pred. No. 0.00037;
Matches 46; Conservative 31; Mismatches 76; Indels 33; Gaps 7;
QY 63 STVQEKQOONISPLVRERGQORVAAHITG-----TEGSRNTLLSPNSKNEKALGRKINS 115
DB 42 SAAQPAKQH-PPKHLANGTUKPAHLVGDPTDPSLRWRANT-----DRAFLR---- 88
QY 116 WESSRSGHSLNHLNGLANGELVHEKGFYIYSQTYFRFQEEIKENTKNDKQWQVYIYKY 175
DB 89 -----HGFL-----LSNNLLVPTSGLYFVYSQVVSFSGEGCFPKATPTPLVAHEVQLF 137
QY 176 TS-YPDILLMKSRNSCWSDAEVGLXSIYOGGIFELKENDRIFSVYTNHEHLIDMDHEA 234
DB 138 SSQYFFHVLPLLSAQSVCPOQPGW-VRSVIQAVFLITCGDQLSTHTDGTGTHLLSPSS 196
QY 235 SFFCAF 240
DB 197 VFFCAF 202

RESULT 8

A25451
tumor necrosis factor alpha precursor - rabbit
N:Alternate names: cachectin; TNF alpha
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 04-Feb-2000
C:Accession: A25451; J50727
R:Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, DNA 5, 149-156, 1986

A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for rab
A;Reference number: A25454; MUID:86219711; PMID:3519137
A;Accession: A25454
A;Molecule type: mRNA
A;Residues: 1-234 <ITO>
A;Cross-references: GB:M12845; NID:g165759; PIDN:AAA31486.1; PID:g165760
R;Ito, H.; Shirai, T.; Yamamoto, S.; Akita, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
DNA 5, 157-165, 1996
A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
A;Reference number: A25451; MUID:86219712; PMID:3519138
A;Accession: A25451
A;Molecule type: DNA
A;Residues: 1-234 <IT2>
A;Note: this sequence differs from that shown in having a Gln inserted between residues
R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-
A;Reference number: JH0309; MUID:91065534; PMID:2249779
A;Accession: J50727
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-62, 'Q', 63-234 <SHA>
A;Cross-references: GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31484.1; PID:g165756
C;Genetics:
A;Introns: 62/3; 80/1; 96/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F;1-81/Domain: propeptide #status predicted <PRO>
F;78-234/Product: tumor necrosis factor #status predicted <MAT>
F;82-234/Binding site: myristate (Lys) (covalent) #status predicted
F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;147-178/Disulfide bonds: #status predicted

Query Match 10.2%; Score 131.5; DB 1; Length 234;
Best Local Similarity 22.9%; Pred. No. 0.00079;
Matches 50; Conservative 36; Mismatches 79; Indels 53; Gaps 10;

QY 29 PNDESMNSPCWQVQKQLRQLVRKMI-LRTSEETISTVOEKQKQINSLVRRGQPRVAAH 87
DB 58 POEESPN-----LHLVNPVQVMTLRSASRALSD-----KPL-----AH 93
QY 88 ITGTGRNTLSSPNKNEKALGRKINSWESSRSHSFLNLHNRGLVTHKGFYIY 147
DB 94 VVA-----NPQVEGQL-----QWLSORANALLANGWLTNDLVLPADGLIY 137
QY 148 SQTYFRFQBEIKENTKQWQVYIYKY-TSPYDPFLLMKSGARNSCWSKDAEYG-----L 201
DB 138 SQVLFSGQ-----GCRSYVLLTHTVSRFAVSYPNKVNLLSAISKSPCHRETPPEAPMAWY 192

QY 202 YSIYGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 238
DB 193 EPIYLGGVFQLEKGRDLSTEVNQPEYDLAESGQVYFG 230

RESULT 9
tumor necrosis factor alpha precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: S12606; S17290; S18965; I46659
R;Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
Nucleic Acids Res. 18, 5564, 1990
A;Title: Gene sequence of porcine tumor necrosis factor alpha.
A;Reference number: S12606; MUID:91016861; PMID:2216741
A;Accession: S12606
A;Molecule type: DNA
A;Residues: 1-232 <DRE>
A;Cross-references: EMBL:X54001; NID:g2135; PIDN:CAA37949.1; PID:g2136
R;Kuhert, P.; Wuehrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal
A;Reference number: S17289; MUID:91340150; PMID:197444
A;Accession: S17290

A;Molecule type: DNA
A;Residues: 1-232 <KHU>
A;Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134
R;Choi, C.S.; Mollitor, T.W.; Lin, G.F.; Murtough, M.P.
submitted to the EMBL Data Library, January 1991
A;Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis
A;Reference number: S18965
A;Accession: S18965
A;Molecule type: mRNA
A;Residues: 1-232 <CHO>
A;Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138
R;Pauli, U.; Beutler, B.; Peterhans, E.
Gene 81, 185-191, 1989
A;Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain react
A;Reference number: I46659; MUID:90034181; PMID:2478420
A;Accession: I46659
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 44-232 <PAU>
A;Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695
C;Genetics:
A;Introns: 62/3; 78/1; 93/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
F;1-77/Domain: propeptide #status predicted <PRO>
F;78-232/Product: tumor necrosis factor alpha #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;144-176/Disulfide bonds: #status predicted

Query Match 10.1%; Score 130; DB 1; Length 232;
Best Local Similarity 25.1%; Pred. No. 0.0011;
Matches 43; Conservative 30; Mismatches 78; Indels 20; Gaps 6;

QY 80 GPORVAHITGTGRSNTLSSPNS---KNEKALGRKINSWESSRSHSFLNLHNRGL 136
DB 66 GLSLINFLAQLRSSQTSDFKVAHVAVNVAEGQL--QWQSYANALLANGWLTNDLV 123
QY 137 VHKQFYIYQTYFRFQBEIKEN---TKNDKQWQVYIYKYTSPYDPFLLMKSGARNSCW 193
DB 124 VVPTDGLYIYQVLFRRGQCPSTVFLTHTSRIA-----VSQTKVNLLSAISKSPCQ 177
QY 194 SK-----DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 238
DB 178 RETPEGAERKPNVEPIYLGVLGVFQLEKDRLSAEINLPDYLDPAESQVYFG 228

RESULT 10
I54490
tumor necrosis factor alpha precursor - white-footed mouse
C;Species: Peromyscus leucopus (white-footed mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 04-Feb-2000
C;Accession: I54490
R;Crew, M.D.; Filipowsky, M.E.
Immunogenetics 35, 351-353, 1992
A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus 1
A;Reference number: I54490; MUID:92218012; PMID:1348497
A;Accession: I54490
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-235 <RES>
A;Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507
C;Genetics:
A;Gene: pLTNF
A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted

Query Match 10.1%; Score 129.5; DB 2; Length 235;
Best Local Similarity 24.5%; Pred. No. 0.0012;

Matches 45; Conservative 39; Mismatches 75; Indels 25; Gaps 9;

QY 72 ISPLVRGPGORVAHITGTRGRSNTL-SSNSKNEKALGRKINSWE-----SSRSGH 123
 Db 56 IGPORERKFPNNLP--IIGSMAQTLLRSSQSSDKFVAHVAVHQAQDEQLEWLSRGA 113

QY 124 SPLSN-LHLRNGELVHEKGFYIYSQTYFRFOBEIKENTKNDKQMVQYIKY-TSYDPD 181
 Db 114 ALLANGMDLKNQVLVPADGLYLVISQVLFKQ-----GCSYVLLHTVSRFAVSVEDEK 168

QY 182 ILLKMSARNSCWSDAEY-----LYSIYGGIFELKENDRIFVSVTNEHLIDMDHEAS 235
 Db 169 VNLLSAIKSPC-PKETPESELKPWYPIYLGGVQLEKGRLSAEVNLKPYLDFAESGQ 227

QY 236 -FFG 238
 Db 228 VYFG 231

RESULT 11
 S24641
 Lymphotoxin - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: I46046; S24641
 R:Clusters, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
 Cytokine 5, 336-341, 1993
 A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tu
 A:Reference number: I46046; MUID:94083525; PMID:8260599
 A:Accession: I46046
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-204 <CL2>
 A:Cross-references: EMBL:Z14137; NID:G796; PIDN:CAA78510.1; PID:G797
 C:Genetics:
 A:Introns: 32/3; 68/1
 C:Superfamily: tumor necrosis factor

Query Match 9.9%; Score 127.5; DB 1; Length 204;
 Best Local Similarity 24.9%; Pred. No. 0.0015;
 Matches 47; Conservative 29; Mismatches 78; Indels 35; Gaps 9;

QY 61 TISTVQEKQNISPLVRGPGORVAHITG-----TRGRSNTLSSPNSKNEKALGRKI 113
 Db 40 TPSAAQPAHQCL-PTPTFTGTLKPAHLVGDPTQDSLWRANT-----DRAFLR-- 88

QY 114 NSWESSRSGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFOBEIKENTKNDKQMVQYIY 173
 Db 89 -----HGF-----SLSNLSLLVPTSGLYFYVSQVWFSGRCGFPRAIPTPLYLAEVQ 135

QY 174 KYT-SYDPDILLKMSARNSCWSDAEYGLYIYGGIFELKENDRIFVSVTN-EHLIDMD 231
 Db 136 LFSFQVFFHVLPLLSAQKSCVCPGQGPW-VRSVYQGAFFLLTRGDQLSTHTDGIHLL-L 193

QY 232 HEASFFGAF 240
 Db 194 PSSVFFGAF 202

RESULT 12
 JQ1344
 tumor necrosis factor alpha precursor - horse
 N:Alternate names: cachectin; TNF alpha
 C:Species: Equus caballus (domestic horse)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
 C:Accession: JQ1344
 R:Su, X.; Morris, D.D.; McGraw, R.A.
 Gene 107, 319-321, 1991
 A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis f
 A:Reference number: JQ1344; MUID:92084125; PMID:1748301
 A:Accession: JQ1344
 A:Molecule type: DNA
 A:Residues: 1-234 <SUX>

A:Cross-references: GB:M64087; NID:G164244; PIDN:AAA30959.1; PID:G164245
 C:Comment: This protein is an important proximal mediator of endotoxemia.
 C:Genetics:
 A:Gene: TNF-alpha
 A:Introns: 62/3; 79/1; 95/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
 F:76-234/Product: tumor necrosis factor alpha #status Predicted <TUM>
 F:19, 20/Binding site: myristate (Lys) (covalent) #status Predicted
 F:82/Binding site: carbohydrate (Ser) (covalent) #status Predicted
 F:146-178/Disulfide bonds: #status Predicted

Query Match 9.8%; Score 126; DB 1; Length 234;
 Best Local Similarity 22.5%; Pred. No. 0.0023;
 Matches 45; Conservative 35; Mismatches 72; Indels 48; Gaps 9;

QY 62 ISTVQEKQ-----QNTISPLVR-----ERGP-QRVAHITGTRGRSNTLSSPNSKNEKALG 110
 Db 56 IGPORERKFPNNLP--IIGSMAQTLLRSSRTPSDKPAHVAV-----NQPAEG 101

QY 111 RKNWESSRSGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFOBEIKENTKNDKQMVQ 170
 Db 102 QL-QWLSGRANALLANGVKLTQNLVPLDGLYIYSQVLFKQ-----GCPSTH 150

QY 171 YIYKT-----SYPPILLKMSARNSCWSDAEY-----LYSIYGGIFELKENDRIF 219
 Db 151 VLLTHTISRAVSYPSKVNLSAIPCHTESPEQAEKQWYPIYLGGVQLEKGDQLS 210

QY 220 VSVTNEHLIDMDHEAS-FFG 238
 Db 211 AEINQPNYLDFAESGQVYFG 230

RESULT 13
 QWUN
 tumor necrosis factor alpha precursor [validated] - human
 N:Alternate names: cachectin; TNFA
 C:Species: Homo sapiens (man)
 C>Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000
 C:Accession: A93585; S36153; A33351; A44189; B61478; I53311; S62610; I54522; A01646; I
 R:Newlin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica
 Nucleic Acids Res. 13, 6361-6373, 1985
 A:Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and c
 A:Reference number: A93585; MUID:86016093; PMID:2995927
 A:Accession: A93585
 A:Molecule type: DNA
 A:Residues: 1-233 <NSD>
 A:Cross-references: GB:X02910; GB:X02159; NID:G37209; PIDN:CAA26669.1; PID:G37210
 R:Irish, P.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Ju
 Nature Genet. 3, 137-145, 1993
 A:Title: Dense Alu clustering and a potential new member of the NFkappaB family withi
 A:Reference number: S36152; MUID:93272029; PMID:8499947
 A:Accession: S36153
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-233 <IRI>
 A:Cross-references: EMBL:Z15026; NID:G37211; PIDN:CAA78745.1; PID:G37212
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
 R:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M
 Nature 312, 724-729, 1984
 A:Title: Human tumour necrosis factor: precursor structure, expression and homology t
 A:Reference number: A93351; MUID:85086244; PMID:6392892
 A:Accession: A93351
 A:Molecule type: mRNA
 A:Residues: 1-233 <PEN>
 A:Cross-references: GB:X02910; GB:X02159; NID:G37209; PIDN:CAA26669.1; PID:G37210
 A:Note: this protein was isolated from the monocytic-like cell line HL-60 from a promy
 R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Aredell, J.N
 Science 228, 149-154, 1985
 A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
 A:Reference number: A44189; MUID:85142190; PMID:3856324
 A:Accession: A44189
 A:Molecule type: mRNA

Lymphokine Res. 7, 175-185, 1988
A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A;Reference number: A61478; MUID:88301617; PMID:2841543
A;Accession: A61478
A;Molecule type: protein
A;Residues: 56-79;86-95,'X',97,'X',99;119-151,'XX',154-162,'X',164,'X',166,'X',168,'X',1
P;Voigt, C.G.; Maurer-Poggy, I.; Adolf, G.R.
FEBS Lett. 314, 85-88, 1992
A;Title: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosylatic
A;Reference number: S26951; MUID:93083656; PMID:1451807
A;Accession: S26951
A;Molecule type: protein
A;Residues: 35-59,'N',61-205 <VOI>
A;Note: 60-Thr was also found
R;Fukushima, K.; Watanabe, H.; Takeo, K.; Nomura, M.; Asahi, T.; Yamashita, K.
Arch. Biochem. Biophys. 304, 144-153, 1993
A;Title: N-linked sugar chain structure of recombinant human lymphotoxin produced by CHO
A;Reference number: S34742; MUID:93311995; PMID:8323280
A;Accession: S34742
A;Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after induction,
while having no detrimental effect on normal cells. It can also act synergistically with
C;Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of differ
ical activities but are produced by different cell types and have different induction ki
C;Genetics:
A;Gene: GDB:LTFA; LT; TNFB
A;Cross-references: GDB:120442; OMIM:153440
A;Map position: 6p21.3-6p21.3
A;Introns: 33/3; 69/1
A;Note: the first intron occurs before the initiator codon
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lymphokine; macrophage
F;1-34/Domain: signal sequence #status predicted <SIG>
F;35-205/Product: lymphotoxin #status predicted <MAT>
F;41/Binding site: carboxylate (Thr) (covalent) #status experimental
F;96/Binding site: carboxylate (Asn) (covalent) #status experimental
Query Match 9.5%; Score 122; DB 1; Length 205;
Best Local Similarity 23.4%; Pred. No. 0.0043;
Matches 37; Conservative 29; Mismatches 72; Indels 20; Gaps 5;
QY 85 AAHTGPRGNTLSNPSNKKVKGKINSWSSRSGHFLSNLHRLNGELVHIEKGFY 144
DB 64 AALHIGDPKQNSL-----LWANTDRAFLQDGFSLNNSLLVPTSGIY 107
QY 145 YIVSQTVFRPQBEIKENTKNDKQWQVYKYTS-YDPILLMKSGARNSWDAEYGLVS 203
DB 108 FVYSQVVFSGKAYSPKATSSPLVLAHEVQLFSSQYFHPVLL-SSQXWVYVGLQEPWLHS 166
QY 204 IYQGIPELXENDRIFVSVIN-BHLIDMDHEAGFFGAF 240
DB 167 MYGAALQLTQGDQLSTHTDGIPLV-LSPSTVFFGAF 203
RESULT 15
QWNSN
Tumor necrosis factor alpha precursor - mouse
N;Alternate names: cachectin; TNF alpha
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 04-Feb-2000
C;Accession: A22908; S03791; A23703; A25164; A34251; I59058; A36696
R;Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
DNA 7, 193-201, 1988
A;Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis
A;Reference number: A22908; MUID:88224564; PMID:2836146
A;Accession: A22908
A;Molecule type: DNA
A;Residues: 1-235 <SHR>
R;Shakhov, A.N.; Nedospasov, S.A.
Bioorg. Khim. 13, 701-705, 1987
A;Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucl
A;Reference number: S03791; MUID:87298639; PMID:3040015
A;Accession: S03791

A;Molecule type: DNA
A;Residues: 1-235 <SHA>
A;Cross-references: GB:M38296; NID:G202086; PIDN:AAA40459.1; PID:G202087
A;Note: article in Russian with English abstract
R;Semion, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor
A;Reference number: A93679; MUID:88067722; PMID:3684584
A;Accession: A93679
A;Molecule type: DNA
A;Residues: 1-235 <SEM>
A;Cross-references: GB:X00467; NID:G54830; PIDN:CAA68530.1; PID:G54832
R;Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985
A;Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necr
A;Reference number: A25164; MUID:85298296; PMID:3898078
A;Accession: A25164
A;Molecule type: mRNA
A;Residues: 1-235 <PEN>
A;Cross-references: GB:M11731; NID:G202084; PIDN:AAA40458.1; PID:G202085
R;Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashim
Nucleic Acids Res. 13, 4417-4429, 1985
A;Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic ex
A;Reference number: A23127; MUID:85242112; PMID:2989794
A;Accession: A23127
A;Molecule type: mRNA
A;Residues: 1-235 <FRA>
A;Cross-references: GB:X02611; NID:G54844; PIDN:CAA26457.1; PID:G54845
R;Cseh, K.; Beutler, B.
J. Biol. Chem. 264, 16256-16260, 1989
A;Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide resul
A;Reference number: A34251; MUID:89380231; PMID:2777790
A;Accession: A34251
A;Molecule type: protein
A;Residues: 70-87 <CSB>
R;Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A;Title: Identification of a common nucleotide sequence in the 3'-untranslated region
A;Reference number: I59058; MUID:86149365; PMID:2419912
A;Accession: I59058
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-230,'R',232-235 <RES>
A;Cross-references: GB:M33049; NID:G202082; PIDN:AAA40457.1; PID:G202083
R;Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
A;Title: Characterization of high molecular weight glycosylated forms of murine tumor
A;Reference number: A36696; MUID:91097531; PMID:2268312
A;Accession: A36696
A;Molecule type: protein
A;Residues: 80-85,'X',87-99 <SHE>
C;Genetics:
A;Introns: 62/3; 81/1; 97/1
A;Note: the first intron occurs in the 5'-untranslated region
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
F;80-235/Product: tumor necrosis factor #status experimental <MAT>
F;20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carboxylate (Ser) (covalent) #status predicted
F;96/Binding site: carboxylate (Asn) (covalent) #status predicted
F;148-179/Disulfide bonds: #status predicted
Query Match 9.4%; Score 121; DB 1; Length 235;
Best Local Similarity 23.1%; Pred. No. 0.0063;
Matches 43; Conservative 34; Mismatches 79; Indels 30; Gaps 8;
QY 67 EKQONISPLVRRGQRVAHITGRGNTLSNP-----NSKNEKALGRKINSWESSR 120
DB 62 EKFPNGLEPLI-----SSMAQTILRSSQNSDKPKVAHVANHQVEEQ 111
QY 121 SGHSFLSNLHRLNGELVHIEKGFYIYQTVFRPQBEIKENTKNDKQWQVYKYT-SYP 179
DB 112 ANALLANGNDLKDQNLVVPADGLYLVYQVLFKQ-----GCPDVLTLTHTVSRFAISVQ 166

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OM protein - protein search, using sw model

Run on: June 3, 2004, 08:53:00 ; Search time 46 Seconds
(without alignments)
1666.759 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281

Perfect score: 1287

Sequence: 1 TNELKMQDKYSGKSIACFL.....NEHLIDMDHEASFFGAFILVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_nhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	879	68.3	287	11	Q8K3G0
2	703.5	54.7	304	13	Q7T1F2
3	307.5	23.9	317	13	Q7ZX9
4	305.5	23.7	214	13	Q9DDZ5
5	305	23.7	287	13	Q9DWT9
6	184.5	14.3	279	11	Q7TMV9
7	180	14.0	252	11	Q8K3Y8
8	176.5	13.7	280	6	Q861W5
9	175.5	13.6	169	11	Q9WV90
10	175	13.6	252	11	Q80Y20
11	173	13.4	252	11	Q8K3Y7
12	166	12.9	251	4	Q8NFE9
13	157	12.2	154	6	Q8MJ19
14	151.5	11.8	227	13	Q7TQ3
15	144.5	11.2	216	11	O70332
16	141	11.0	231	13	Q8AW02

17	137.5	10.7	232	11	Q80XA4
18	135	10.5	156	11	Q91ZL4
19	135	10.5	215	6	Q9BEE8
20	135	10.5	217	11	Q9BER6
21	130.5	10.1	222	13	Q7TLU4
22	128	9.9	230	13	Q8G37
23	127	9.9	253	13	Q7T194
24	126.5	9.8	225	13	Q91B42
25	125	9.7	215	11	Q99ND1
26	124	9.6	216	6	Q9BEC4
27	123.5	9.5	216	6	Q9BEC9
28	122	9.5	205	4	Q8N4C3
29	121.5	9.4	225	13	Q91B41
30	121.5	9.4	246	13	Q91976
31	121.5	9.4	246	13	Q91970
32	120	9.3	237	13	Q8AWC9
33	119	9.2	202	11	Q80WE7
34	115.5	9.0	149	6	Q97543
35	113.5	8.8	255	13	Q91810
36	113.5	8.8	255	13	Q9DEF9
37	110.5	8.6	217	6	Q9BEG0
38	110	8.5	93	6	Q9TTU2
39	109.5	8.5	149	6	Q97538
40	109.5	8.5	149	6	Q9TTG8
41	108.5	8.4	214	6	Q9BEF3
42	108	8.4	103	6	Q864Y7
43	108	8.4	217	6	Q9BEG1
44	107	8.3	217	6	Q9BEF4
45	106.5	8.3	102	11	Q80Z06

ALIGNMENTS

RESULT 1

Q8K3G0 PRELIMINARY; PRT; 287 AA.
 ID Q8K3G0
 DT 01-OCT-2002 (TRENBLrel. 22, Created)
 DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE TNF-related apoptosis inducing ligand.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DA;
 RA Mueller A.M., Giegerich G.;
 RT "Rattus norvegicus TNF-related apoptosis inducing ligand (TRAIL).";
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY115578; AAM49797.1;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS0049; TNF_2; 1.
 SQ SEQUENCE 287 AA; 32979 MW; CA4F5B5D7C833FEC CRC64;

Query Match 68.3%; Score 879; DB 11; Length 287;

Best Local Similarity 59.7%; Pred. No. 1,6e-65;

Matches 170; Conservative 25; Mismatches 43; Indels 6; Gaps 2;

QY 2 NELKMQDKYSGKSIACFLKEDSDYNDENDESMNSPCWQVQRLVRQMLTSET 61

DB 44 NEVKQLQDNYSKIGLACFSKEDGDFWSDTEGILNRPCLQVQRQLYIEVTLRTFT 103

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QY 62 ISTVQKQVNIPLVREGRQVAAHITGRSNTLSPNSKNEKALGRKINSWESSRS 121
DB 104 ISTVPEKQLSTPLPRGRPRQVAAHITGRSNTLSPNSKNEKALGRKINSWESSRS 163
QY 122 GHSFLSNLHRLNGELVHKGFFYYISQYFFQOE--EIKENTKD----KQWQVYIKY 175
DB 164 GHSFLNHLVRLNGELVHKGFFYYISQYFFQOE--EIKENTKD----KQWQVYIKY 223
QY 176 TSPYDPILLMKSNRNSWCKDAEYGLYSYQGGIFELKENDRIFVSVNEHLMDHEAS 235
DB 224 TSPYDPILLMKSNRNSWCKDAEYGLYSYQGGIFELKENDRIFVSVNEHLMDHEAS 283
QY 236 FFGA 239
DB 284 FFGA 287

RESULT 2
Q7T1F2 PRELIMINARY; PRT; 304 AA.
AC Q7T1F2;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DE Tumor necrosis factor related apoptosis inducing ligand.
GN TRAIL.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Syed A.A., Horiuchi H.H., Furusawa S., Matsuda H.;
RT "Identification and Characterization of Chicken TNF-Superfamily
RT Ligand 8 (CD30 Ligand) and 10 (Tumor Necrosis Factor Related Apoptosis
RT Inducing Ligand TRAIL).";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB114678; BAC79267.1; -.
SQ SEQUENCE 304 AA; 34658 MW; DFC128B517747C96 CRC64;

Query Match 54.7%; Score 703.5; DB 13; Length 304;
Best Local Similarity 54.7%; Pred. No. 8.2e-51;
Matches 141; Conservative 40; Mismatches 58; Indels 19; Gaps 6;

QY 1 TNELKQWQVNIPLVREGRQVAAHITGRSNTLSPNSKNEKALGRKINSWESSRS 121
DB 36 TNELKQWQVNIPLVREGRQVAAHITGRSNTLSPNSKNEKALGRKINSWESSRS 163
QY 56 RTSETISTVQ-EKQNIPLVREGRQVAAHITGRSNTLSPNSKNEKALGRKINSWESSRS 110
DB 96 RILQNNNSAINGDRTOALS-RDEPPQGTPLAIAHLTGSKRSSA-SPHNYLSYRGIG 152
QY 111 RKINSWESSRSGHFLNHLRNGELVHKGFFYYISQYFFQOE-----IKENTKN 164
DB 153 HKHSWESSRSGHFLNHLRNGELVHKGFFYYISQYFFQOE-----IKENTKN 212
QY 165 DKQWQVNIPLVREGRQVAAHITGRSNTLSPNSKNEKALGRKINSWESSRS 224
DB 213 PKQLVQVYIKLTYNPDILLMKSNRNSWCKDAEYGLYSYQGGIFELKENDRIFVSVN 272
QY 225 EHLMDHEASFFGAFLV 242
DB 273 SDIVMDKEASFFGAFLV 290

RESULT 3
Q7ZYX9 PRELIMINARY; PRT; 317 AA.
AC Q7ZYX9;
DT 01-JUN-2003 (Tremblrel. 24, Created)
```

```
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to tumor necrosis factor (ligand) superfamily, member 10.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN 1;
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC044336; AAH44336.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SMO0207; TNF; 1.
DR PROSITE; PS00049; TNF; 1.
SQ SEQUENCE 317 AA; 35465 MW; 68F76BC1A40DCB9F CRC64;

Query Match 23.9%; Score 307.5; DB 13; Length 317;
Best Local Similarity 29.8%; Pred. No. 1.2e-17;
Matches 77; Conservative 50; Mismatches 96; Indels 35; Gaps 8;

QY 1 TNELKQWQVNIPLVREGRQVAAHITGRSNTLSPNSKNEKALGRKINSWESSRS 121
DB 73 TEELRCL-----GLNLVGLKQDI--PEDLAQLFGPCMKLAEGIKAVISKVTDISI 123
QY 54 -----ILRTSEETISTVQ-EKQNIPLVREGRQVAAHITGRSNTLSPNSKNEKALGRKINSWESSRS 103
DB 124 KQTLHAARTHTSYNTGSKFWTV-----MQPSAHLTLSSASNSRPSQDMHQPF 176
QY 104 KNEKALGRKINSWESSRSGHFLNHLRNGELVHKGFFYYISQYFFQOEIKENT 162
DB 177 DLHQCRRHPVHTW-ANKSFGAHLNMTLTNGLRVDPQDGRYYISQYFFPSDSQDS 235
QY 163 KNDKQWQVNIPLVREGRQVAAHITGRSNTLSPNSKNEKALGRKINSWESSRS 222
DB 236 SVSHQLVQCIYKTSYLNPLQLLKGVTGKWPADAEALHSVYOGGLFELRAGDEVFVS 295
QY 223 TNEHLIDMDHEASFFGAFLV 240
DB 296 SSPTWYGEDSSSYFGAF 313

RESULT 4
Q9DDZ5 PRELIMINARY; PRT; 214 AA.
AC Q9DDZ5;
DT 01-NAR-2001 (Tremblrel. 16, Created)
DT 01-NAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE TRAIL-like protein.
GN TNFSF10L.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN 1;
RP SEQUENCE FROM N.A.
RA Bobe J., Goetz F.W.;
RT "Molecular cloning and expression of a TNF receptor and two TNF
RT ligands in the fish ovary."
RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481 (2001).
DR EMBL; AF250041; AAG47640.1; -.
DR HSSP; P50591; 1DQO.
DR ZFIN; ZDB-GENE-010801-1; tnfsf10l.
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DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00049; TNF 2; 1.
SQ SEQUENCE 214 AA, 24093 MW, 98C002474FF691AA CRC64;

Query Match      23.7%; Score 305.5; DB 13; Length 214;
Best Local Similarity 37.6%; Pred. No. 1.1e-17;
Matches 62; Conservative 37; Mismatches 59; Indels 7; Gaps 3;

QY 82 QRVAHITGRGRNT-----LSSPNKNEKALGRKINSWSSRSGHSLNHLRNGEL 136
DB 47 QAPSAHLTSSASDNSRQSDHQFDLHSCRPVHTW-ANKSFGAHLNWTLTNGRL 105

QY 137 VIHEKGFYIYSQTYFRF-QEEIKENTKNDKQMVQIYKTSYPPDLLMKSARNCSWK 195
DB 106 RVPQDGRVYLYSÖVYFRYSPSDSQSSVSHQVQCIYKTSYLNPIQLLKGVGTKWAP 165

QY 196 DAEYGLYSYGGIFELKENDRIFVSTNEHLIDMDHEASFFGAF 240
DB 166 DAYALSHSVYQGLPELRAGDEVFVSVSPTVMVYGEDSSSYFGAF 210

RESULT 5
Q30WT9 PRELIMINARY; PRT; 287 AA.
ID Q30WT9;
AC Q30WT9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TNF-related apoptosis inducing ligand.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OC NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Bridgham J.T., Johnson A.L.;
RT "TNF-related apoptosis inducing ligand (TRAIL) expression in the hen ovary."
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY057941; AAL23702.1; -.
DR HSSP; O35235; 1IQA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF_subf.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECRCSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00049; TNF 2; 1.
SQ SEQUENCE 287 AA, 32092 MW, DB061C95087B108 CRC64;

Query Match      23.7%; Score 305; DB 13; Length 287;
Best Local Similarity 33.7%; Pred. No. 1.7e-17;
Matches 84; Conservative 40; Mismatches 97; Indels 28; Gaps 8;

QY 8 QDKYSGGIACFLKEDSDYWDNDDESM-NSPCQVQWQLRQLVRKMLRTSEET--ST 64
DB 47 QSQSGSEELRCLQLNQOQSGSLEELISNQC-----LKLANTIKAYATVTENVISRSV 102

QY 65 VQEQKQ---NISP-LVRERGPQVAAHI-----TGTRGRNTLSSPNSGKNEKALGR 111

us-10-662-430-2_copy_39_281.open.rspt
DB 103 VNEAQSYFNISEGQVATKTLGKPSAHLIFRPNQPAQDGSSRRFNGLS-----QSCRH 155
QY 112 KINSWESSRSGHSLNHLRNGELVTHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQY 171
DB 156 AITRWEDS-TIHLQNITRDGLRVNQAGKYVYVSIYFYPSRDGAGARVSPQLVQC 214
QY 172 IYKYTSYPPDLLMKSARNCSWKDAEYGLYSYGGIFELKENDRIFVSTNEHLIDMD 231
DB 215 INWKTSYQFILLKGVGTCKWAPAEYGLHALYQGLFELKAGDELFFVSVSSLAIDYSD 274
QY 232 HEASFFGAF 240
DB 275 AASFFGAF 283

RESULT 6
Q7TMV9 PRELIMINARY; PRT; 279 AA.
ID Q7TMV9;
AC Q7TMV9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Tnsf6 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapellato M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Besak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6NCR; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052866; AAH52866.1; -.
SQ SEQUENCE 279 AA, 31416 MW, C2972E2728FEBB7B CRC64;

Query Match      14.3%; Score 184.5; DB 11; Length 279;
Best Local Similarity 25.3%; Pred. No. 2e-07;
Matches 50; Conservative 51; Mismatches 64; Indels 33; Gaps 9;

QY 45 QLRQLVRKMLRTSEETISTVQEQKQNIPLVRERGPQVAAHITGRSNTLSSPNSK 104
DB 111 ELREFTNQSL-----KVSSFQKQIANPSTPEKPEPSV-AHUTG-----NPHSR 154

QY 105 NEKALGRKINSWSSRSGHSLNHLRNGELVTHEKGFYIYSQTYFRFQEEIKENTKN 164
DB 155 SIPL-----EWET-YGTALISGVKYKGLVLNETGLYFVSKVFRGQ-----SCN 201

QY 165 DKQMVQYIY-KYTSYPPDLLMKSAR-NSCWKDAEYGLYSYGGIFELKENDRIFVSV 222
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Db 202 NQPLAHKVMRSKYPEDLVMEERLNYCTT--GQIWAHSHLGAVENTLTSADHLVNI 259
QY 223 TNEHLIDMDHEASFFGAF 240
Db 260 SLSLINFESKTFGLY 277

RESULT 7
O8K3Y8
ID O8K3Y8 PRELIMINARY; PRT; 252 AA.
AC O8K3Y8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TNF superfamily ligand TL1A.
GN TNFSF15.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; PubMed=11911831;
RX MEDLINE=21909416; Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
RA Migone T.S., Zhang J., Luo X., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,
RA Perry J.W., Chen S.F., Olsen H.S., Hu G., Fukac L.S., Liu D., Ni J.,
RA Carrell J., Boyd E., Olsen H.S., Hu G., Fukac L.S., Liu D., Ni J.,
RA Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;
RT "TL1A is a TNF-like ligand for DR3 and TR6/DR3 and functions as a T
RT cell costimulator.";
RL Immunity 16:479-492(2002).
DR EMBL; AF520786; AAM7367.1; -.
DR MGD; MGI:2180140; Tnfslf15.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF-like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF 2; 1.
SQ SEQUENCE 252 AA; 27723 MW; BB901C9350119E0F CRC64;

Query Match 14.0%; Score 180; DB 11; Length 252;
Best Local Similarity 32.4%; Pred. No. 4.1e-07;
Matches 69; Conservative 26; Mismatches 80; Indels 36; Gaps 12;

QY 45 QLRLVRLKMLRTSEETISTVQKQNIPLVREGRPQVAAHITGRGRSNTLSPNSK 104
Db 63 QLAVPGKDCMLRAITRERSE-PSFQVYSP---PRGKPR--AHLT-----IKQTAPHLX 112
QY 105 NE-KALGRKINSWESSRSGHSFLN-LHLRNGELVTHEKGFIYYSQTYFRQEEI---- 158
Db 113 NQLSAL-----HWEHD-LGVAFTKMGKYNKSLVIPESGDYFIYSQITFRGTTSYCGDI 166
QY 159 ---KENTKDKQVQYIY-KYTSYDPDILLMK-SARNSC-----WSKDAEYGLYSIYGGIF 210
Db 167 SRGRPNKPSITVITVKYVADSPPEARLLTGSKSVCESNNW-----FQSLVIGANF 219
QY 211 ELKENDRIFVSVTNEHLIDMDHE-ASFFGAFV 242
Db 220 SLEEGRLMNVSDISLVDTYKEDKTFPGAFLL 252

RESULT 8
O861W5
ID O861W5 PRELIMINARY; PRT; 280 AA.
AC O861W5;
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DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fas ligand.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99053606; PubMed=9839871;
RA Mizuno T., Endo Y., Momoi Y., Goto Y., Nishimura Y., Taubota K.,
RA Mikami T., Ohno K., Matsui T., Tsujimoto H., Hasegawa A.;
RT "Molecular cloning of feline Fas antigen and Fas ligand cDNAs.";
RL Vet. Immunol. Immunopathol. 65:161-172(1998).
DR EMBL; AB009280; BAC76426.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR008983; TNF-like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR ProDom; PD01234; TNCRSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS50049; TNF 2; 1.
SQ SEQUENCE 280 AA; 31361 MW; 6AA7E2DB1F1A6B5C CRC64;

Query Match 13.7%; Score 176.5; DB 6; Length 280;
Best Local Similarity 26.9%; Pred. No. 9.2e-07;
Matches 56; Conservative 48; Mismatches 63; Indels 41; Gaps 12;

QY 44 WQLRQLVRKMI-LR--TSBETISTVQKQ-QNISPLVREGRPQVAAHITGRGRSNTLS 99
Db 101 FQLFHLQELAEALRETSQKHVASSLEKQIQLNPPSEKRLKV-AHLTG----- 150
QY 100 SPNSKNEKALGRKINSWESSRSGHSFLN-LHLRNGELVTHEKGFIYYSQTYFRQEEIK 159
Db 151 KPNRSRIPL-----EWEDT-YGIALVSGVKYKKGGLVINDTGMFYFVKVNRFGQ---- 199
QY 160 ENTNDKQVQYIY-KYTSYDPDILLMK-SARNSC-----WSKDAEYGLYSIYGGIFEL 212
Db 200 --SCNQLNKHVTRNSKTPQDLVLNKGMMQVCTTGQWNR-----SSVLGAVFNL 250
QY 213 KENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 251 TSADHLVNVSELSVFSFESSKTFGLY 278

RESULT 9
O9WV90
ID O9WV90 PRELIMINARY; PRT; 169 AA.
AC O9WV90;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Fas ligand (Fragment).
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
```

RX MEDLINE=20010026; PubMed=10540161;
RA Hodgson P.D., Grant M.D., Michalak T.I.;
RT "Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and
RT chronic woodchuck viral hepatitis";
RL Clin. Exp. Immunol. 118:63-70(1999).
DR EMBL; AF152368; AAD33387.1; -
DR HSSP; P50591; ID4V.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0005915; P:apoptosis; IEA.
DR GO; GO:0004955; P:immune response; IEA.
DR GO; GO:000165; P:signal transduction; IEA.
DR InterPro; IPR008084; Fas_ligand.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
FT NON_TER 1
FT NON_TER 169
SQ SEQUENCE 169 AA; 19274 MW; FDE395B014717B6B CRC64;

Query Match 13.6%; Score 175.5; DB 11; Length 169;
Best Local Similarity 27.8%; Pred. No. 5.9e-07;
Matches 54; Conservative 39; Mismatches 58; Indels 43; Gaps 10;

QY 45 QLRQVVKMLRTSEETISVQKQNIPLVREPGPQVAAHITGRGRNTLSPNSK 104
DB 10 ELRESNQ---RWTEPSL-----EKQICHPSSPSDKALRAAHLT---GKPSRSP---- 56
QY 105 NEKALGRKINSWESSRSGHSFLNLHRLNGELVIHEKGFYIYQSYFQBEIKENTKN 164
DB 57 -----LEWEDT-YGISLISGVKYQKGLVINDTGLYFVYSKIYFRGQ-----SCN 100
QY 165 DKQMVQYIY-KYTSYDPDILLMK-SARNSC-----WSKDAEYGLYIYGGIFELKENDR 217
DB 101 NQPLSHKVVYVKNKYFQDLVIMBGMVKNYCTTCQMMAR-----SSYLGAVFNTSNDH 153
QY 218 IFVSVTNEHLIDMD 231
DB 154 LYVNVSELSUINFE 167

RESULT 10
Q80YZO PRELIMINARY; PRT; 252 AA.
AC Q80YZO;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE B20K13.3 (Tumor necrosis factor (ligand) superfamily, member 15).
DE 15).
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Sycamore N.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL691468; CAD83021.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0003164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0005915; P:immune response; IEA.
DR InterPro; IPR006053; TNF_subf.
DR InterPro; IPR008983; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 252 AA; 28029 MW; 7789B6556D46F293 CRC64;

DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 252 AA; 27725 MW; A63ABDC9E96E0F CRC64;

Query Match 13.6%; Score 175; DB 11; Length 252;
Best Local Similarity 31.9%; Pred. No. 1.1e-06;
Matches 68; Conservative 26; Mismatches 81; Indels 38; Gaps 12;

QY 45 QLRQVVKMLRTSEETISVQKQNIPLVREPGPQVAAHITGRGRNTLSPNSK 104
DB 63 QLRVFGKDCMLRAITEERSE-PSFQVYSP---PRGKPR--AHLT-----IKKOTPAHLK 112
QY 105 NE-KALGRKINSWESSRSGHSFLSN-LHLRNGELVIHEKGFYIYQSYFQBEI---- 158
DB 113 NQLSAL-----HWEHD-LGMAFTKMGKYNKLSVIPESGDYFIYSQITPRGTTCVCGDI 166
QY 159 ---KENTKNDKQMVQYIYKYTSYDPDILLMKSNRSC-----WSKDAEYGLYIYQGGIF 210
DB 167 SRGRPNKPDSTITVITKVADSYPEPARLITGSKSVCEISNNW-----FQSLYLGAFT 219
QY 211 ELKENDRIFVSVTNEHLIDMDHE-ASPFAPLV 242
DB 220 SLEGGDLVNVSDISLVDTYKEDKTFEGALL 252

RESULT 11
Q8K3Y7 PRELIMINARY; PRT; 252 AA.
AC Q8K3Y7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE TNF superfamily ligand TLIA.
GN TNFSF15.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley;
RC MEDLINE=21909416; PubMed=11911831;
RA Migone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
RA Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,
RA Carrell J., Boyd S.F., Olsen H.S., Hu G., Pukac L., Liu D., Ni J.,
RA Kim S., Gentz R., Feng P., Moore P.A., Ruben S.M., Wei P.;
RT "TLIA is a TNF-like ligand for DR3 and TR6/Dcr3 and functions as a T cell costimulator."
RL Immunity 16:479-492(2002).
DR EMBL; AF520787; AAM77368.1; -
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF_subf.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNCRSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 252 AA; 28029 MW; 7789B6556D46F293 CRC64;

Query Match 13.4%; Score 173; DB 11; Length 252;
Best Local Similarity 32.7%; Pred. No. 1.6e-06;
Matches 56; Conservative 23; Mismatches 62; Indels 30; Gaps 8;

QY 86 AHITGRGRNTLSPNSKNEKALGRKINSWESSRSGHSFLSN-LHLRNGELVIHEKGFY 144

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Db 98 AHLTINR-----QTPVHLKNELA-----ALHWNEN-LGMAFTKRMVNTNKNFLVIFESGDY 148
QY 145 YIYSQYFRFQ-----BEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNSC-----192
Db 149 FYISQITFRGTSECDISRVPRKPPDSITVITKVDVSYEPHAHLTGTKSCVISESN 208
QY 193 WSKDAEYGYISYQGGIFELKENDRIFVSVTNEHLIDMDHE-ASFFGAFLV 242
Db 209 W-----FQPIYLGAMFSLIEGDRLMNVNSDISLVDYTKEDKTFGAFLI 252

RESULT 12
Q8MJ19 PRELIMINARY; PRT; 251 AA.
AC Q8MJ19;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE TNF superfamily ligand TLIA.
GN TNFSF15.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21909416; PubMed=11911831;
RA Migone T.S., Zhang J., Luo X., Zhuang L., Chen C., Hu B., Hong J.S.,
RA Perry J.W., Chen S.F., Zhou J.X., Cho Y.H., Ullrich S., Kanakaraj P.,
RA Carrell J., Boyd E., Olsen H.S., Hu G., Pukac L., Liu D., Ni J.,
RA Kim S., Gentz R., Peng P., Moore P.A., Ruben S.M., Wei P.;
RT "TLIA is a TNF-like ligand for DR3 and TR3/DcR3 and functions as a T
RT cell costimulator";
RL Immunity 16:479-492(2002).
DR EMBL; AF520785; AAM77366.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF-like.
DR InterPro; IPR001636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR ProDom; PD002012; TNF_subf; 1.
DR PRINTS; PR01234; TNFCROSISFCT.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS50049; TNF 2; 1.
SQ SEQUENCE 251 AA; 28087 MW; 65ED70E367E3446D CRC64;

Query Match 12.9%; Score 166; DB 4; Length 251;
Best Local Similarity 33.2%; Pred. No. 6.1e-06;
Matches 62; Conservative 30; Mismatches 65; Indels 30; Gaps 12;

QY 69 QQNISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNE-KALGKINSWESSRSGHSFLS 127
Db 82 QQVAPLRADGDKPR--AHITVVR-----QPTQHRKNQFPAL-----HWE-HELGLAFTK 129

QY 128 N-LHLRNGELVIHEKGYIYSQTYFRFQ---BEIKENTKNDK--QMVQYIYKYT-SYP 179
Db 130 NRMVNTNKNFLIPESGDYFYVSQVTPRGMTSECEIRQAGRPKNKPDSTIWTIKVTDSTYP 189

QY 180 DPILLMKSARNSCWSDAEGV---LVSIIYGGIFELKENDRIFVSVTNEHLIDMDHE-AS 235
Db 190 EPTOLLNGTKSVSC-----EVGSNWFQPIYLGAMFSLQEGDKLMNVNSD:SLVDYTKEDKT 244

QY 236 FFGAFLV 242
Db 245 FFGAFL 251

RESULT 13
Q8MJ19 PRELIMINARY; PRT; 154 AA.
AC Q8MJ19;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Fas ligand CD178 (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Petit F., Arnoult D., Lelievre J.-D., Lecossier D., Hance A.J.,
RA Monceaux V., Ho Tsong Fang R., Hurtrel B., Ameisen J.-C.,
RA Estaquier J.;
RT "Caspase-dependent and -independent cell death pathways characterize
RT pathogenic Simian Immunodeficiency Virus infection. Relationship with
RT disease evolution";
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF530076; AAM95836.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007155; P:signal transduction; IEA.
DR InterPro; IPR008064; Fas_ligand.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF-like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF 2; 1.
FT NON TER 1
FT NON TER 154
SQ SEQUENCE 154 AA; 17410 MW; 971A43779E029449 CRC64;

Query Match 12.2%; Score 157; DB 6; Length 154;
Best Local Similarity 27.4%; Pred. No. 1.9e-05;
Matches 46; Conservative 33; Mismatches 65; Indels 24; Gaps 6;

QY 57 TSEETISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSW 116
Db 8 TSQKHTASSLEKQIGHPSPPEKKEQKVAHLTG-----KPNRSRML-----EW 52

QY 117 ESSRSRSHSFLNHLRNGELVIHEKGYIYSQTYFRFQBEIKENTKNDKQMVQYIY-KY 175
Db 53 EDT-YGIVLLSGVKYKGGVLINETGLYFVYSKYVFRGQ-----SCTNLP LSHKVYWRN 105

QY 176 TSYDPDPILLMKSARNSCWSDAEGVLYSIYGGIFELKENDRIFVSVT 223
Db 106 SKYFQDLVMEGKQMS-YCTTGQWVAHSSVILGAVFNLT SADHLVNVVS 152

RESULT 14
Q7T2Q3 PRELIMINARY; PRT; 227 AA.
AC Q7T2Q3;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Tumor necrosis factor-3 alpha.
GN TNF-3ALPHA.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinus.
OX NCBI_TaxID=7962;
RN [1]
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RP SEQUENCE FROM N.A.
RC TISSUE=Head kidney;
RA Sazan R., Sakai M.;
RT "Cloning of tumor necrosis factor 3 alpha in carp.";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB112424; BAC77690.1;
SQ SEQUENCE 227 AA; 25226 MW; 010BC2B1E8D7265E CRC64;

Query Match 11.8%; Score 151.5; DB 13; Length 227;
Best Local Similarity 25.3%; Pred. No. 8.7e-05;
Matches 45; Conservative 34; Mismatches 68; Indels 31; Gaps 7;

QY 75 LVRRGPGQVAHITGTRGNTLLSPNSKNEKALGRKINSWESSRSGHSLNHLRNG 134
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 67 LSKENVTSKVAIHLSGA-----YEPDVSKNNIDWKQNDQGAFFVSGGLKLVDR 113
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 135 ELVIHEKGYIYTSQYFRFOEIKENTKNDKQWQYIYKYSYD-----PILLMKSA 188
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 EIIIPNDGIYTSQVSPHI--SKNDMTEDQEVNHHVSHAVFYHSDFFGIYKP--LIRAA 169
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 189 RNSCW----SKDAEGLYIYGGIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF 240
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 170 RSACVHASNTEDVWD--TIYLGAAFSLRAGDKLCTKTTELLPRVETDNAKTFGVF 225
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
O70332 PRELIMINARY; PRT; 216 AA.
AC O70332;
DT 01-AUG-1998 (TRENBLrel. 07, Created)
DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Tumor necrosis factor-alpha (Fragment).
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=98234044; PubMed=9573100;
RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
analysis of cytokine mRNA expression in experimental visceral
leishmaniasis.";
RL Infect. Immun. 66:2135-2142(1998).
DR EMBL; AF046215; AAC40100.1;
DR HSP; P06804; 2TNF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNFCROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS0049; TNF 2; 1.
FT NON_TER 1
FT NON_TER 216
SQ SEQUENCE 216 AA; 23793 MW; BADA3F83F45B533 CRC64;
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Query Match 11.2%; Score 144.5; DB 11; Length 216;
Best Local Similarity 26.9%; Pred. No. 0.00032;
Matches 47; Conservative 28; Mismatches 63; Indels 37; Gaps 7;
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QY 80 GPQVAAH---ITGTRGNTL--SSPNSKNEKALGRKINS-----WESSRSGHSL 127
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 49 GPQREKFPNPIIGSQTLTLLRSSQNSNDKPGVHVANHOVEQLEWLSHRANALIAN 108
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
QY 128 NLHLRNGELVIHEKGYIYTSQYFRFOEIKENTKNDKQWQYIYK-----VTSYD 180
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 109 GMSLKDNQIVIPADGLYLVYSQVLFPGQ-----GCPSYVLLTHTVSRIVASYED 157
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 181 PILLMKSAARNSCWSKDAEYGV-----LYSIYGGIFELKENDRIFVSVTNEHLID 229
   : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 158 NVNLLISAIXSPC-PKETPEGEELKPYEPIYLGGVFQLEKGDRLSAENVLPKYLD 211
   : : : : : : : : : : : : : : : : : : : : : : : : : :
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Search completed: June 3, 2004, 08:55:46
Job time : 48 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2004, 11:29:46 ; Search time 48 Seconds
(without alignments)
1424.277 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281

Perfect score: 1287
Sequence: 1 TNELKQMDKYSKSGTACFL.....NEHLIDMDHEASFFGALVIG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 1155919

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1287	100.0	279	13	US-10-066-209-3
2	1287	100.0	281	8	US-08-916-625B-6
3	1287	100.0	281	8	US-08-971-317A-8
4	1287	100.0	281	9	US-09-813-329-17
5	1287	100.0	281	9	US-09-193-663-8
6	1287	100.0	281	9	US-09-934-465-1
7	1287	100.0	281	10	US-09-919-039-118
8	1287	100.0	281	12	US-10-202-062-20
9	1287	100.0	281	12	US-10-662-429-2
10	1287	100.0	281	12	US-10-662-430-2
11	1287	100.0	281	12	US-10-662-431-2
12	1287	100.0	281	12	US-10-652-244-2
13	1287	100.0	281	12	US-10-279-687-8
14	1287	100.0	281	13	US-10-039-785-66
15	1287	100.0	281	13	US-10-011-125-4

16	1287	100.0	281	13	US-10-001-054-54
17	1287	100.0	281	14	US-10-093-766-54
18	1287	100.0	281	14	US-10-174-654-11
19	1287	100.0	281	14	US-10-151-882-41
20	1287	100.0	281	14	US-10-218-547-20
21	1287	100.0	281	14	US-10-322-673-72
22	1287	100.0	281	14	US-10-139-785-66
23	1287	100.0	281	14	US-10-310-793-26
24	1287	100.0	281	15	US-10-292-486-5
25	1287	100.0	281	15	US-10-333-712-1
26	1078.5	83.8	246	9	US-09-855-544A-13
27	988	76.8	253	12	US-10-652-244-11
28	988	76.8	256	12	US-10-652-244-13
29	984	76.5	461	12	US-10-389-223A-6
30	982	76.3	480	12	US-10-389-223A-4
31	978	76.0	614	12	US-10-389-223A-2
32	964.5	74.9	296	14	US-10-185-425-5
33	887	68.9	168	9	US-09-900-530A-10
34	878	68.2	166	9	US-09-779-050A-16
35	863	67.1	291	10	US-09-873-829-6
36	863	67.1	291	12	US-10-652-244-6
37	863	67.1	291	13	US-10-017-910-6
38	859	66.7	164	13	US-10-116-378-29
39	850	66.0	161	14	US-10-216-074-7
40	849	66.0	161	14	US-10-338-083-11
41	826	64.2	208	9	US-09-855-544A-16
42	746.5	58.0	188	9	US-09-855-544A-14
43	636	49.4	172	9	US-09-779-050A-17
44	446	34.7	85	14	US-10-286-696-12
45	370	28.7	113	9	US-09-855-544A-15

ALIGNMENTS

RESULT 1
US-10-066-209-3
; Sequence 3, Application US/10066209
; Publication No. US20020115110A1
; GENERAL INFORMATION:
; APPLICANT: Brigham-Burke, Michael R.
; APPLICANT: Young, Peter R.
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030-D1
; CURRENT APPLICATION NUMBER: 09/072,993
; PRIOR FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 09/072,993
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-10-066-209-3

Query March 100.0%; Score 1287; DB 13; Length 279;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGTACFLKEDDSYDPNDESNMSPCWQVKQRLQRLVRKMLRTSSE 60
Db 37 TNELKQMDKYSKSGTACFLKEDDSYDPNDESNMSPCWQVKQRLQRLVRKMLRTSSE 96
QY 61 TISTVQEKQNTSPLVREGRGPORVAHITGTGRNTLSSPNKKEKALGRKINWESSR 120

Db 97 TISTVQEQKQNISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 156
QY 121 SGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRQOEIKENTKNDKQVQIYKYTSYD 180
Db 157 SGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRQOEIKENTKNDKQVQIYKYTSYD 216
QY 181 PILLKMSARNCSWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 217 PILLKMSARNCSWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 276
QY 241 LVG 243
Db 277 LVG 279

RESULT 2

US-08-916-625B-6
; Sequence 6, Application US/08916625B
; Publication No. US20010010924A1
; GENERAL INFORMATION:
; APPLICANT: DEEN, KEITH C.
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RELATED
; TITLE OF INVENTION: RECEPTOR, TR6
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATNER & PRESTIA
; STREET: P.O. BOX 980
; CITY: VALLEY FORGE
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/916.625B
; FILING DATE: 22-AUG-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/853,684
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: 60/041,230
; FILING DATE: 14-MARCH-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: PRESTIA, PAUL F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-50008-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-916-625B-6

Query Match 100.0%; Score 1287; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESNNSPCWQVKQLRQVLRKMLRTSEE 60
Db 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESNNSPCWQVKQLRQVLRKMLRTSEE 98
QY 61 TISTVQEQKQNISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120

Db 99 TISTVQEQKQNISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRQOEIKENTKNDKQVQIYKYTSYD 180
Db 159 SGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRQOEIKENTKNDKQVQIYKYTSYD 218
QY 181 PILLKMSARNCSWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLKMSARNCSWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
Db 279 LVG 281

RESULT 3

US-08-971-317A-8
; Sequence 8, Application US/08971317A
; Publication No. US20010010925A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971.317A
; FILING DATE: 17-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goller, Mini C
; REGISTRATION NUMBER: 39,046
; REFERENCE/DOCKET NUMBER: 6255.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 935-7550
; TELEFAX: (847) 938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20010010925A1e
US-08-971-317A-8

Query Match 100.0%; Score 1287; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESNNSPCWQVKQLRQVLRKMLRTSEE 60
Db 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESNNSPCWQVKQLRQVLRKMLRTSEE 98
QY 61 TISTVQEQKQNISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEQKQNISPLVRERGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVTHEKGFYIYSQTYFRQOEIKENTKNDKQVQIYKYTSYD 180


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Db 159 SCHSFLSNLHRLNGELVTHKGFYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYD 218
Qy 181 PILLMKSARNCSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Qy 241 LVG 243
Db 279 LVG 281

RESULT 4
US-09-813-329-17
; Query Match 100.0%; Score 1287; DB 9; Length 281;
; Best Local Similarity 100.0%; Pred. No. 1.9e-115;
; Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; ORGANISM: Drosophila melanogaster
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: No. US20020012968A1el Drosophila Tumor Necrosis Factor Class Mole
; TITLE OF INVENTION: Variants Thereof
; FILE REFERENCE: D0016.np
; CURRENT APPLICATION NUMBER: US/09/813,329
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 60/190,816
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 17
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-813-329-17

Query Match 100.0%; Score 1287; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDESMNSPCWQVQWLQRLVRKMLRTSEE 60
Db 39 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDESMNSPCWQVQWLQRLVRKMLRTSEE 98
Qy 61 TISTVQEKQONISPLVREGRGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVREGRGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
Qy 121 SCHSFLSNLHRLNGELVTHKGFYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYD 180
Db 159 SCHSFLSNLHRLNGELVTHKGFYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYD 218
Qy 181 PILLMKSARNCSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Qy 241 LVG 243
Db 279 LVG 281

RESULT 5
US-09-193-663-8
; Query Match 100.0%; Score 1287; DB 9; Length 281;
; Best Local Similarity 100.0%; Pred. No. 1.9e-115;
; Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; ORGANISM: Homo sapiens
; GENERAL INFORMATION:
; APPLICANT: Willey, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255.US.02
; CURRENT APPLICATION NUMBER: US/09/193,663
; CURRENT FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/065,916
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
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; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-663-8

Query Match 100.0%; Score 1287; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDESMNSPCWQVQWLQRLVRKMLRTSEE 60
Db 39 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDESMNSPCWQVQWLQRLVRKMLRTSEE 98
Qy 61 TISTVQEKQONISPLVREGRGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVREGRGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
Qy 121 SCHSFLSNLHRLNGELVTHKGFYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYD 180
Db 159 SCHSFLSNLHRLNGELVTHKGFYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYD 218
Qy 181 PILLMKSARNCSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Qy 241 LVG 243
Db 279 LVG 281

RESULT 6
US-09-934-465-1
; Query Match 100.0%; Score 1287; DB 9; Length 281;
; Best Local Similarity 100.0%; Pred. No. 1.9e-115;
; Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; ORGANISM: Homo sapiens
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/09/934,465
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: 08/584,031
; PRIOR FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-934-465-1

Query Match 100.0%; Score 1287; DB 9; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDESMNSPCWQVQWLQRLVRKMLRTSEE 60
Db 39 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDESMNSPCWQVQWLQRLVRKMLRTSEE 98
Qy 61 TISTVQEKQONISPLVREGRGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVREGRGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
Qy 121 SCHSFLSNLHRLNGELVTHKGFYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYD 180
Db 159 SCHSFLSNLHRLNGELVTHKGFYIYSQTYFRFOEIKENTKNDKQVQIYKYTSYD 218
Qy 181 PILLMKSARNCSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Qy 241 LVG 243
Db 279 LVG 281
```

```
RESULT 7
US-09-919-039-118
; Sequence 118, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 059509CDI
US-09-919-039-118

Query Match 100.0%; Score 1287; DB 10; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEE 98

QY 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHLRANGELVIEHKGFIYISQTYFRFQBEIKENTKNDKQMVYIYKTSYD 180
DB 159 SGHSFLSNLHLRANGELVIEHKGFIYISQTYFRFQBEIKENTKNDKQMVYIYKTSYD 218

QY 181 PILLMKSARNCSWSDAEGLYSIYOGGIFELKENDRIFSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWSDAEGLYSIYOGGIFELKENDRIFSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
DB 279 LVG 281

RESULT 8
US-10-202-062-20
; Sequence 20, Application US/10202062
; Publication No. US20040038349A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.,
; TITLE OF INVENTION: Heteromultimeric TNF Ligand Family members
; FILE REFERENCE: PF559
; CURRENT APPLICATION NUMBER: US/10/202,062
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,838
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-202-062-20

Query Match 100.0%; Score 1287; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEE 98

QY 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHLRANGELVIEHKGFIYISQTYFRFQBEIKENTKNDKQMVYIYKTSYD 180
DB 159 SGHSFLSNLHLRANGELVIEHKGFIYISQTYFRFQBEIKENTKNDKQMVYIYKTSYD 218

QY 181 PILLMKSARNCSWSDAEGLYSIYOGGIFELKENDRIFSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWSDAEGLYSIYOGGIFELKENDRIFSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
DB 279 LVG 281

RESULT 9
US-10-662-429-2
; Sequence 2, Application US/10662429
; Publication No. US20040038347A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M
; TITLE OF INVENTION: Apoptosis Inducing Molecule I
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/662,429
; APPLICATION NUMBER: US/10/662,429
; FILING DATE: 16-Sep-2003
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/816,981
; FILING DATE: 13-Mar-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Kimball, Paul, C.
; REGISTRATION NUMBER: 34,610
; REFERENCE/DOCKET NUMBER: PF261
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-662-429-2

Query Match 100.0%; Score 1287; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSGKSGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRQLVRKMLRTSEE 98
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QY 61 TISTVQEKQNTISPLVRERGPORVAHAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
 Db 99 TISTVQEKQNTISPLVRERGPORVAHAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFSLNHLRNGELVIEHKGFFYYISQTYFRFOEIKENTKNDKQWQVYIKYTSYD 180
 Db 159 SGHSFSLNHLRNGELVIEHKGFFYYISQTYFRFOEIKENTKNDKQWQVYIKYTSYD 218
 QY 181 PILLMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 Db 219 PILLMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 Db 279 LVG 281

RESULT 10
 US-10-662-430-2
 ; Sequence 2, Application US/10662430
 ; Publication No. US20040048340A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben, Steven M
 ; TITLE OF INVENTION: Apoptosis Inducing Molecule I
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/662,430
 ; FILING DATE: 16-Sep-2003
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/816,981
 ; FILING DATE: 13-MAR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kimball, Paul, C.
 ; REGISTRATION NUMBER: 34,610
 ; REFERENCE/DOCKET NUMBER: PF261
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 281 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-662-430-2

Query Match 100.0%; Score 1287; DB 12; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.9e-115;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYSKSGIACFLKEDDSYDPNDEESMNSPCWQVQWQLRQLVVKMLRTSEE 60
 Db 39 TNELKQMDKYSKSGIACFLKEDDSYDPNDEESMNSPCWQVQWQLRQLVVKMLRTSEE 98
 QY 61 TISTVQEKQNTISPLVRERGPORVAHAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
 Db 99 TISTVQEKQNTISPLVRERGPORVAHAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFSLNHLRNGELVIEHKGFFYYISQTYFRFOEIKENTKNDKQWQVYIKYTSYD 180
 Db 219 PILLMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 Db 279 LVG 281

Db 159 SGHSFSLNHLRNGELVIEHKGFFYYISQTYFRFOEIKENTKNDKQWQVYIKYTSYD 218
 QY 181 PILLMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 Db 219 PILLMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 Db 279 LVG 281
 RESULT 11
 US-10-662-431-2
 ; Sequence 2, Application US/10662431
 ; Publication No. US20040047864A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben, Steven M
 ; TITLE OF INVENTION: Apoptosis Inducing Molecule I
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: US
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/662,431
 ; FILING DATE: 16-Sep-2003
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/816,981
 ; FILING DATE: 13-MAR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kimball, Paul, C.
 ; REGISTRATION NUMBER: 34,610
 ; REFERENCE/DOCKET NUMBER: PF261
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 281 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-10-662-431-2

Query Match 100.0%; Score 1287; DB 12; Length 281;
 Best Local Similarity 100.0%; Pred. No. 1.9e-115;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYSKSGIACFLKEDDSYDPNDEESMNSPCWQVQWQLRQLVVKMLRTSEE 60
 Db 39 TNELKQMDKYSKSGIACFLKEDDSYDPNDEESMNSPCWQVQWQLRQLVVKMLRTSEE 98
 QY 61 TISTVQEKQNTISPLVRERGPORVAHAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
 Db 99 TISTVQEKQNTISPLVRERGPORVAHAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFSLNHLRNGELVIEHKGFFYYISQTYFRFOEIKENTKNDKQWQVYIKYTSYD 180
 Db 159 SGHSFSLNHLRNGELVIEHKGFFYYISQTYFRFOEIKENTKNDKQWQVYIKYTSYD 218
 QY 181 PILLMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240

Db 219 PILLKMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
Qy 241 LVG 243
|||
Db 279 LVG 281

RESULT 12

US-10-652-244-2
; Sequence 2, Application US/10652244
; Publication No. US20040052789A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-652-244-2

Query Match 100.0%; Score 1287; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGGIACFLKEDDSYDNDDESMNSPCWQVKQLRQLVRKMLRTSEE 60
|||
Db 39 TNELKQMDKYSGGIACFLKEDDSYDNDDESMNSPCWQVKQLRQLVRKMLRTSEE 98
|||
Qy 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 120
|||
Db 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 158
|||
Qy 121 SGHSFLNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQWQIYKYTSYD 180
|||
Db 159 SGHSFLNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQWQIYKYTSYD 218
|||
Qy 181 PILLKMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
|||
Db 219 PILLKMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
|||
Qy 241 LVG 243
|||
Db 279 LVG 281

RESULT 13

US-10-279-687-8
; Sequence 8, Application US/10279687
; Publication No. US20030211509A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF

; FILE REFERENCE: 6255.US.C2
; CURRENT APPLICATION NUMBER: US/10/279,687
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 10/105,738
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/193,663
; PRIOR FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US 60/065,916
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-279-687-8

Query Match 100.0%; Score 1287; DB 12; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGGIACFLKEDDSYDNDDESMNSPCWQVKQLRQLVRKMLRTSEE 60
|||
Db 39 TNELKQMDKYSGGIACFLKEDDSYDNDDESMNSPCWQVKQLRQLVRKMLRTSEE 98
|||
Qy 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 120
|||
Db 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 158
|||
Qy 121 SGHSFLNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQWQIYKYTSYD 180
|||
Db 159 SGHSFLNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQWQIYKYTSYD 218
|||
Qy 181 PILLKMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
|||
Db 219 PILLKMSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
|||
Qy 241 LVG 243
|||
Db 279 LVG 281

RESULT 14

US-10-039-785-66
; Sequence 66, Application US/10039785
; Publication No. US20020067646A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 66
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
US-10-039-785-66

Query Match 100.0%; Score 1287; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 98

QY 61 TISTVQEKQNISPLVRERGQPVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQNISPLVRERGQPVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHRLNGELVIEHKGFFYYISQTYFRFQEEIKENTKNDKQWQYIYKYTSYDP 180
DB 159 SGHSFLSNLHRLNGELVIEHKGFFYYISQTYFRFQEEIKENTKNDKQWQYIYKYTSYDP 218

QY 181 PILLKMSARNCSWKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLKMSARNCSWKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
DB 279 LVG 281

RESULT 15
US-10-011-125-4
Sequence 4, Application US/10011125
Publication No. US20020142388A1
GENERAL INFORMATION:
APPLICANT: Chen, Christina Yu-Ching
TITLE OF INVENTION: BACTERIAL HOST STRAINS
FILE REFERENCE: F1804K1
CURRENT APPLICATION NUMBER: US/10/011.125
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: US 60/256,162
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 4
LENGTH: 281
TYPE: PRT
ORGANISM: Homo sapiens
US-10-011-125-4

Query Match 100.0%; Score 1287; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 98

QY 61 TISTVQEKQNISPLVRERGQPVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQNISPLVRERGQPVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHRLNGELVIEHKGFFYYISQTYFRFQEEIKENTKNDKQWQYIYKYTSYDP 180
DB 159 SGHSFLSNLHRLNGELVIEHKGFFYYISQTYFRFQEEIKENTKNDKQWQYIYKYTSYDP 218

QY 181 PILLKMSARNCSWKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLKMSARNCSWKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
DB 279 LVG 281

RESULT 16
US-10-001-054-54
Sequence 54, Application US/10001054
Publication No. US20020192209A1
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Baker, Kevin
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Hebert, Carolyn
APPLICANT: Henzel, William
APPLICANT: Kabakoff, Rhona
APPLICANT: Shelton, David
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin
APPLICANT: Wood, William
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING NEOPLASTIC
TITLE OF INVENTION: CELL GROWTH
FILE REFERENCE: P3034R1PCT
CURRENT APPLICATION NUMBER: US/10/001.054
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 60/059114
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/079689
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/079920
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/085149
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/090691
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/096891
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/096894
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: 60/099803
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100263
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: 60/100390
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/101476
PRIOR FILING DATE: 1998-09-23
PRIOR APPLICATION NUMBER: 60/107783
PRIOR FILING DATE: 1998-11-10
PRIOR APPLICATION NUMBER: 60/108849
PRIOR FILING DATE: 1998-11-18
PRIOR APPLICATION NUMBER: 60/112420
PRIOR FILING DATE: 1998-12-15
PRIOR APPLICATION NUMBER: 60/113296
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/115554
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115558
PRIOR FILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 60/115533
PRIOR FILING DATE: 1999-01-20
PRIOR APPLICATION NUMBER: 60/123618
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: 60/131294
PRIOR FILING DATE: 1999-04-07
PRIOR APPLICATION NUMBER: 60/140650
PRIOR FILING DATE: 1999-06-22

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; PRIOR APPLICATION NUMBER: 60/141037
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/144758
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 60/187202
; PRIOR FILING DATE: 2000-03-03
; PRIOR APPLICATION NUMBER: 60/209832
; PRIOR FILING DATE: 2000-06-05
; PRIOR APPLICATION NUMBER: 60/232887
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: 09/180997
; PRIOR FILING DATE: 1998-11-19
; PRIOR APPLICATION NUMBER: 09/218517
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 09/284291
; PRIOR FILING DATE: 1999-04-12
; PRIOR APPLICATION NUMBER: 09/380137
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380138
; PRIOR FILING DATE: 1999-08-25
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; PRIOR FILING DATE: 1999-09-09
; PRIOR APPLICATION NUMBER: 09/403297
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 09/423741
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: 09/709238
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 09/802706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 09/866034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/872035
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 09/882636
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 09/924419
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/927796
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: 09/929404
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 09/941992
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/946374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: PCT/US98/18824
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/US99/00106
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/08615
; PRIOR FILING DATE: 1999-04-20
; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28634
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: PCT/US99/30095

; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00376
; PRIOR FILING DATE: 2000-01-06
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/04342
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/06884
; PRIOR FILING DATE: 2000-03-15
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: 2000-03-30
; PRIOR APPLICATION NUMBER: PCT/US00/13705
; PRIOR FILING DATE: 2000-05-17
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US00/14941
; PRIOR FILING DATE: 2000-05-30
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/22031
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: PCT/US01/06666
; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: PCT/US01/27099
; PRIOR FILING DATE: 2001-08-29
; NUMBER OF SEQ ID NOS: 91
; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-001-054-54

Query Match      100.0%; Score 1287; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  TNELKQMDKYSGKSGIACFLKEDDSYWDNDDESNPCWQVKWQLRQLVRKMLRTSEE 60
Db      39  TNELKQMDKYSGKSGIACFLKEDDSYWDNDDESNPCWQVKWQLRQLVRKMLRTSEE 98
Qy      61  TISTVOEKQNTSPLVRERGQPVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSR 120
Db      99  TISTVOEKQNTSPLVRERGQPVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSR 158
Qy      121 SGHSFLSNLHLRNGELVIEHKGFFYIYSQTYFRFOBEIKENTKNDKQWQYIYKYTSYD 180
Db      159 SGHSFLSNLHLRNGELVIEHKGFFYIYSQTYFRFOBEIKENTKNDKQWQYIYKYTSYD 218
Qy      181 PILLKMSARNSCWSCDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
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|||||
Db 219 PILLMKSARNCSWCKDAEYGLSYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
|||
Db 279 LVG 281

RESULT 17
US-10-093-766-54
; Sequence 54, Application US/10093766
; Publication No. US20030013099A1
; GENERAL INFORMATION:
; APPLICANT: Lasek, Amy W.
; APPLICANT: Jones, David A.
; APPLICANT: Karpf, Adam R.
; TITLE OF INVENTION: GENES REGULATED BY DNA METHYLATION IN COLON TUMORS
; FILE REFERENCE: PA-0047 US
; CURRENT APPLICATION NUMBER: US/10/093,766
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PERL Program
; SEQ ID NO 54
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; FEATURE:
; OTHER INFORMATION: Incyte ID No. US20030013099A1 059509CD1
US-10-093-766-54

Query Match 100.0%; Score 1287; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLMILRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLMILRTSEE 98

QY 61 TISTVQEKQNI SPLVREGRQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQNI SPLVREGRQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRQEEIKENTKNDKQMVQIYKYTSYD 180
Db 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRQEEIKENTKNDKQMVQIYKYTSYD 218

QY 181 PILLMKSARNCSWCKDAEYGLSYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSWCKDAEYGLSYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
|||
Db 279 LVG 281

RESULT 18
US-10-174-654-11
; Sequence 11, Application US/10174654
; Publication No. US20030044937A1
; GENERAL INFORMATION:
; APPLICANT: Bienkowski, Michael J
; APPLICANT: Mills, Cynthia J
; APPLICANT: Jones, David A
; TITLE OF INVENTION: TNF-Related Death Ligand
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pharmacia & Upjohn, Intellectual Property
; STREET: 301 Henrietta Street
; CITY: Kalamazoo
; STATE: MI
; COUNTRY: USA
```

```
ZIP: 49001
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/174,654
FILING DATE: 19-Jun-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kerber, Lori L.
REGISTRATION NUMBER: 41,113
REFERENCE/DOCKET NUMBER: 6111.N CN1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 616/833-0974
TELEFAX: 616/833-8897
TELEX: 224401
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-174-654-11

Query Match 100.0%; Score 1287; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLMILRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLMILRTSEE 98

QY 61 TISTVQEKQNI SPLVREGRQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQNI SPLVREGRQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRQEEIKENTKNDKQMVQIYKYTSYD 180
Db 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRQEEIKENTKNDKQMVQIYKYTSYD 218

QY 181 PILLMKSARNCSWCKDAEYGLSYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKSARNCSWCKDAEYGLSYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
|||
Db 279 LVG 281

RESULT 19
US-10-151-882-41
; Sequence 41, Application US/10151882
; Publication No. US20030059862A1
; GENERAL INFORMATION:
; APPLICANT: Ruben, Steven M.
; TITLE OF INVENTION: Antibodies Against Tumor Necrosis Factor Delta (APRIL)
; FILE REFERENCE: PFS54
; CURRENT APPLICATION NUMBER: US/10/151,882
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 60/293,100
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-882-41
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Query Match
Best Local Similarity 100.0%; Score 1287; DB 14; Length 281;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDEESMNSPCQVQKQLRQVVKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDEESMNSPCQVQKQLRQVVKMLRTSEE 98
QY 61 TISTVQEQQNISPVLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEQQNISPVLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSLNHLRNGELVTHEKGFFYYISQTYFRQEEIKENTKNDKQVQVYIKYTSYD 180
DB 159 SGHSFLSLNHLRNGELVTHEKGFFYYISQTYFRQEEIKENTKNDKQVQVYIKYTSYD 218
QY 181 PILLMKSARNCSWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 20
US-10-218-547-20
; Sequence 20, Application US/10218547
; Publication No. US20030100074A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Methods And Compositions For Treating Metabolic Bone Diseases Rel
; TITLE OF INVENTION: Human Endokine Alpha
; FILE REFERENCE: PF561
; CURRENT APPLICATION NUMBER: US/10/218,547
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/312,542
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/330,761
; PRIOR FILING DATE: 2001-10-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-218-547-20

Query Match
Best Local Similarity 100.0%; Score 1287; DB 14; Length 281;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDEESMNSPCQVQKQLRQVVKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDEESMNSPCQVQKQLRQVVKMLRTSEE 98
QY 61 TISTVQEQQNISPVLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEQQNISPVLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSLNHLRNGELVTHEKGFFYYISQTYFRQEEIKENTKNDKQVQVYIKYTSYD 180
DB 159 SGHSFLSLNHLRNGELVTHEKGFFYYISQTYFRQEEIKENTKNDKQVQVYIKYTSYD 218
QY 181 PILLMKSARNCSWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 21
US-10-322-673-72
; Sequence 72, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 72
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-673-72

Query Match 100.0%; Score 1287; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDEESMNSPCQVQKQLRQVVKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDEESMNSPCQVQKQLRQVVKMLRTSEE 98
QY 61 TISTVQEQQNISPVLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEQQNISPVLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSLNHLRNGELVTHEKGFFYYISQTYFRQEEIKENTKNDKQVQVYIKYTSYD 180
DB 159 SGHSFLSLNHLRNGELVTHEKGFFYYISQTYFRQEEIKENTKNDKQVQVYIKYTSYD 218
QY 181 PILLMKSARNCSWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 22
US-10-139-785-66
; Sequence 66, Application US/10139785
; Publication No. US20030190685A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/139,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044

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; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent in ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-139-785-66

Query Match      100.0%; Score 1287; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYKSGIACFLKEDDSYDNDDEESMSPCWQVKWQLRQLVRKMLRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDDSYDNDDEESMSPCWQVKWQLRQLVRKMLRTSEE 98

Qy 61 TISTVQEKQONISPLVREGRPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVREGRPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

Qy 121 SGHSFLNLHLRNGELVHEKGFYIYSQYFRFOEBIKENTKNDKQWQVYIYKTSYPD 180
Db 159 SGHSFLNLHLRNGELVHEKGFYIYSQYFRFOEBIKENTKNDKQWQVYIYKTSYPD 218

Qy 181 PILMKARSNSCWSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILMKARSNSCWSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

Qy 241 LVG 243
Db 279 LVG 281

RESULT 23
US-10-793-793-26
; Sequence 26, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods And Compositions For Treating Inflammatory Bowel Diseases
; TITLE OF INVENTION: Relating to Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: PF573
; CURRENT APPLICATION NUMBER: US/10/310,793
; PRIOR FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
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; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 26
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-10-310-793-26

Query Match      100.0%; Score 1287; DB 14; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYKSGIACFLKEDDSYDNDDEESMSPCWQVKWQLRQLVRKMLRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDDSYDNDDEESMSPCWQVKWQLRQLVRKMLRTSEE 98

Qy 61 TISTVQEKQONISPLVREGRPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVREGRPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

Qy 121 SGHSFLNLHLRNGELVHEKGFYIYSQYFRFOEBIKENTKNDKQWQVYIYKTSYPD 180
Db 159 SGHSFLNLHLRNGELVHEKGFYIYSQYFRFOEBIKENTKNDKQWQVYIYKTSYPD 218

Qy 181 PILMKARSNSCWSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILMKARSNSCWSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

Qy 241 LVG 243
Db 279 LVG 281

RESULT 24
US-10-292-486-5
; Sequence 5, Application US/10292486
; Publication No. US20030228309A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies That Immunospecifically Bind To TRAIL Receptors
; FILE REFERENCE: PF532P1
; CURRENT APPLICATION NUMBER: US/10/292,486
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/403,376
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/377,973
; PRIOR FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/331,309
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 09/986,149
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,359
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/295,018
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/252,904
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/248,847
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: 60/246,612
; PRIOR FILING DATE: 2000-11-08
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 5
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-292-486-5

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Query Match      100.0%; Score 1287; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYKSGIACFLKEDDSYDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 98

QY 61 TISTVQEKQONISPLVRERGPQVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGPQVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHRLNGELVHEKGFYIYSQYFRQBEIKENTKNDKQWQVIYKYTSYD 180
DB 159 SGHSFLSNLHRLNGELVHEKGFYIYSQYFRQBEIKENTKNDKQWQVIYKYTSYD 218

QY 181 PILLKMSARNCSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLKMSARNCSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
DB 279 LVG 281
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RESULT 25

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US-10-333-712-1
; Sequence 1, Application US/10333712
; Publication No. US2004005314A1
; GENERAL INFORMATION:
; APPLICANT: Escandon, Enrique
; APPLICANT: Fox, Judith A.
; APPLICANT: Kelley, Sean K.
; APPLICANT: Xiang, Hong
; TITLE OF INVENTION: APO-2L RECEPTOR AGONIST AND CPT-11 SYNERGISM
; FILE REFERENCE: P1838R1
; CURRENT APPLICATION NUMBER: US/10/333,712
; FILING DATE: 2003-01-23
; PRIOR APPLICATION NUMBER: PCT/US01/23691
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: US 60/221,256
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-333-712-1
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Query Match      100.0%; Score 1287; DB 15; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.9e-115;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYKSGIACFLKEDDSYDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYKSGIACFLKEDDSYDNDDESMNSPCQVKWQLRQLVRKMLRTSEE 98

QY 61 TISTVQEKQONISPLVRERGPQVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGPQVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHRLNGELVHEKGFYIYSQYFRQBEIKENTKNDKQWQVIYKYTSYD 180
DB 159 SGHSFLSNLHRLNGELVHEKGFYIYSQYFRQBEIKENTKNDKQWQVIYKYTSYD 218

QY 181 PILLKMSARNCSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLKMSARNCSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
DB 279 LVG 281
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Db

279 LVG 281

Search completed: June 3, 2004, 11:36:41
Job time : 49 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2004, 09:00:51 ; Search time 20 Seconds
(without alignments)
1168.727 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281

Perfect score: 1287
Sequence: 1 INELKQMDKYKSGIACFL.....NEHLIDMDHASFAGFLVG 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 125680

Minimum DB seq length: 0
Maximum DB seq length: 243

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	134.5	10.5	204	1 S17289	tumor necrosis fac
2	131.5	10.2	234	1 A25451	tumor necrosis fac
3	130	10.1	232	1 S12606	tumor necrosis fac
4	129.5	10.1	235	2 I54490	tumor necrosis fac
5	127.5	9.9	204	1 S24641	lymphotoxin - bovi
6	126	9.8	234	1 JQ1344	tumor necrosis fac
7	123	9.6	233	1 QWJUN	tumor necrosis fac
8	122	9.5	205	1 QWJUX	lymphotoxin alpha
9	121	9.4	235	1 QWJUN	tumor necrosis fac
10	121	9.4	235	2 JU0029	tumor necrosis fac
11	120	9.3	233	1 S22052	tumor necrosis fac
12	117.5	9.1	234	1 JU0529	tumor necrosis fac
13	115.5	9.0	193	2 S06192	tumor necrosis fac
14	114	8.9	202	1 B27303	tumor necrosis fac
15	113.5	8.8	185	2 S52715	tumor necrosis fac
16	113	8.8	233	1 S24642	tumor necrosis fac
17	111.5	8.7	202	1 JU0869	tumor necrosis fac
18	107	8.3	197	1 JU0309	tumor necrosis fac
19	98.5	7.7	233	2 S11688	tumor necrosis fac
20	80.5	6.3	203	2 C89803	conserved hypotet
21	78	6.1	202	2 A82076	hypothetical prote
22	77	6.0	223	2 H71485	peptide transport
23	76.5	5.9	195	2 S77753	dnax suppressor pr
24	75.5	5.9	142	2 B87569	hypothetical prote
25	74	5.7	201	2 B82310	hypothetical prote
26	73	5.7	223	2 B64396	hypothetical prote
27	73	5.7	227	2 B70438	conserved hypotet
28	72.5	5.6	112	2 AF0347	hypothetical prote
29	72.5	5.6	123	2 T26862	hypothetical prote

30	72.5	5.6	156	2 H71623	probable secreted
31	72.5	5.6	218	2 A99014	hypothetical prote
32	72.5	5.6	243	2 A99387	SAM-dependent meth
33	71.5	5.6	195	1 I40422	conserved hypotet
34	71.5	5.6	227	2 H64336	formate dehydrogen
35	71	5.5	234	2 H21543	hypothetical prote
36	70.5	5.5	189	2 D45188	chitin synthase [E
37	70.5	5.5	222	2 T37839	hypothetical prote
38	70.5	5.5	226	2 C81749	conserved hypotet
39	70	5.4	209	2 D90593	lipoprotein import
40	69.5	5.4	144	2 H81292	hypothetical prote
41	69.5	5.4	199	2 JE0351	OX40 ligand protei
42	69.5	5.4	201	2 S53800	chitin synthase [E
43	69.5	5.4	202	2 B90180	ABC transporter, A
44	69.5	5.4	222	2 A81896	hypothetical prote
45	69	5.4	139	2 T28300	ORF MSV139 hypothe

ALIGNMENTS

RESULT 1

S17289
tumor necrosis factor beta precursor - pig
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S17289
R:Kuhnert, P.; Wuehrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A:Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative an
A:Reference number: S17289; MUID:91340150; PMID:1874444
A:Accession: S17289
A:Molecule type: DNA
A:Residues: 1-204 <KUH>
A:Cross-references: EMBL:X54859; NID:G2132; PIDN:CAA38638.1; PID:G2133
C:Genetics:
A:Insertions: 32/3; 68/1
C:Superfamily: tumor necrosis factor
C:Keywords: cytotoxin; glycoprotein; lymphokine; macrophage
F:1-33/Domain: signal sequence #status predicted <SIG>
F:34-204/Product: tumor necrosis factor beta #status predicted <MAT>

Query Match	10.5%	Score 134.5	DB 1	Length 204	
Best Local Similarity	24.7%	Pred. No. C.00037			
Matches	46	Conservative 31	Mismatches 76	Indels 33	Gaps 7
Qy	63	STVQEKQKNISPLVRRGPQORVAAHITG-----TRGRSNTLSSPNSKNEKALGRKINS	115		
Db	42	SAAQPAQH-PPKHLARGTLKPAHLVGDPSTPDSLWRANT-----DRAFLR----	88		
Qy	116	WESSRSQHSFLSNLHNLNGELVTHEKGFYIIYSQTVFRFOEIKENTQDKQWQVIYKY	175		
Db	89	-----HGFL-----LSNNSLLVPTSGLYFYISQVVFSGGCPFKATPTPLYLAHEVOLFL	137		
Qy	176	TS-YPDPILLMKARNCSKDAEYGLYSIQGGIFELKENDRIFSVVTNEHLIDMDHEA	234		
Db	138	SSQYFFVHLLSAQKSVCPGQGPW-VRSYVQAVFLITQGDQLSTHTDTPHLLSPSS	196		
Qy	235	SFFGAF	240		
Db	197	VFFGAF	202		

RESULT 2

A25451
tumor necrosis factor alpha precursor - rabbit
N:Alternate names: cachectin; TNF alpha
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C:Accession: A25451; A25451; J50727
R:Rito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi,
DNA 5, 149-156, 1986
A:Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for

QY 72 ISPLVRGPORVAHIITGTRGRNTL-SSPNSKNEKALGRKINSWE-----SSRSGH 123
 DB 56 IGPOREKFPNNLP--IIGSNAQTLTLRSSQNSGSDKFAVHVAHQVDEQLEWLSRGAN 113
 QY 124 SFLSN-LHLRNGELVIHEKGFYIYSOTYFFRQBEIKENTKNDKQMVYIKY-TSYDDP 181
 DB 114 ALLANGMDLKNQLVIRADGLYVYSQVLFKQ-----GCSYVLLTHTVSRFAVSIEDK 168
 QY 182 ILLMKASRNSCWSKDAEY-----LYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEAS 235
 DB 169 VNLLSAIKSPC-PKETPSGSELKPWVEPIYLGGVFQLEKGRDLGSAEVLNPKYLDFAESGQ 227
 QY 236 -FFG 238
 DB 228 VYFG 231

RESULT 5
 S24641
 Lymphotoxin - bovine
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: I46046; S24641
 R:Clutds, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
 Cytokine 5, 336-341, 1993
 A:Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and tu
 A:Reference number: I46046; MUID:94083525; PMID:8260599
 A:Accession: I46046
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-204 <CL2>
 A:Cross-references: EMBL:214137; NID:g796; PIDN:CAA78510.1; PID:g797
 C:Genetics:
 A:Introns: 32/3; 68/1
 C:Superfamily: tumor necrosis factor

Query Match 9.9%; Score 127.5; DB 1; Length 204;
 Best Local Similarity 24.9%; Pred. No. 0.0015;
 Matches 47; Conservative 29; Mismatches 78; Indels 35; Gaps 9;

QY 61 TISTVQEKQNTISPLVRGPORVAHIITG-----TRGRSNTLSSPNSKNEKALGRKI 113
 DB 40 TPSAAQPAHQQL-PTPTFTGTLKPAHLVGDPTQDSLRWRANT-----DRAFLR-- 88
 QY 114 NSWESSRSGHSPFLSNLHNLNGELVIHEKGFYIYSOTYFFRQBEIKENTKNDKQMVYIY 173
 DB 89 -----HGF-----SLSNLSLLVPTSLGLYFYVYQVYVSGFCPPRAITPTFLYLAHEVQ 135
 QY 174 KTT-SYDPDILLMKASRNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTN-EHLIDMD 231
 DB 136 LFSQPQYFFHVLISLAKSKYCPGQPGW-VRSYVQGAFFLTRGDQLSTHTDGIHLL-LS 193
 QY 232 HEASFFGAF 240
 DB 194 PSSVFFGAF 202

RESULT 6
 JQ1344
 tumor necrosis factor alpha precursor - horse
 N:Alternate names: cachectin; TNF alpha
 C:Species: Equus caballus (domestic horse)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
 C:Accession: JQ1344
 R:Su, X.; Morris, D.D.; McGraw, R.A.
 Gene 107, 319-321, 1991
 A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis f
 A:Reference number: JQ1344; MUID:92084125; PMID:1748301
 A:Accession: JQ1344
 A:Molecule type: DNA
 A:Residues: 1-234 <SUX>
 A:Cross-references: GB:M64087; NID:G164244; PIDN:AAA30959.1; PID:g164245

C:Comment: This protein is an important proximal mediator of endotoxemia.
 C:Genetics:
 A:Gene: TNF-alpha
 A:Introns: 62/3; 79/1; 95/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; me
 F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
 F:19,20/Binding site: myristate (lys) (covalent) #status predicted
 F:82/Binding site: carbohydrate (ser) (covalent) #status predicted
 F:146-178/Disulfide bonds: #status predicted

Query Match 9.8%; Score 126; DB 1; Length 234;
 Best Local Similarity 22.5%; Pred. No. 0.0023;
 Matches 45; Conservative 35; Mismatches 72; Indels 48; Gaps 9;

QY 62 ISTVQEKQ-----QNTISPLVR-----ERGP-QRVAHIITGTRGRSNTLSSPNSKNEKALG 110
 DB 56 IGPOREQLPNAFQSIPLAQLTLSSSRTPSPDKPAHVVA-----NPQAEQ 101
 QY 111 RKINSWESSRSGHSPFLSNLHNLNGELVIHEKGFYIYSOTYFFRQBEIKENTKNDKQMVQ 170
 DB 102 QL--QWLSGRANALLANGVLTNDQVLPDLGLYIYSQVLFKQ-----GCPSTH 150
 QY 171 YIYKYT-----SYDPDILLMKASRNSCWSKDAEY-----LYSIYOGGIFELKENDRIF 219
 DB 151 VLLTHIRSLAYSYPSPKVNLLSAIKSPCHTESPEQAEKXPWVEPIYLGGVFQLEKGDQLS 210
 QY 220 VSVTNEHLIDMDHEAS-FFG 238
 DB 211 AEINQPNYLDFAESGQVYFG 230

RESULT 7
 QW1UN
 tumor necrosis factor alpha precursor [validated] - human
 N:Alternate names: cachectin; TNFA
 C:Species: Homo sapiens (man)
 C>Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000
 C:Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; B
 R:Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica,
 Nucleic Acids Res. 13, 6361-6373, 1985
 A:Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and ch
 A:Reference number: A93585; MUID:86016093; PMID:2995927
 A:Accession: A93585
 A:Molecule type: DNA
 A:Residues: 1-233 <NED>
 A:Cross-references: GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
 R:Iris, F.J.M.; Bougueret, L.; Prieur, S.; Caterina, D.; Perrot, V.; Jur
 Nature Genet. 3, 137-145, 1993
 A:Title: Dense Aliu clustering and a potential new member of the NFkappaB family within
 A:Reference number: S36152; MUID:93272029; PMID:8499947
 A:Accession: S36153
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-233 <TRI>
 A:Cross-references: EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID:g37212
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
 F:Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.
 Nature 312, 724-729, 1984
 A:Title: Human tumour necrosis factor: precursor structure, expression and homology to
 A:Reference number: A93351; MUID:85086244; PMID:6392892
 A:Accession: A93351
 A:Molecule type: mRNA
 A:Residues: 1-233 <PEN>
 A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
 A>Note: this protein was isolated from the monocyte-like cell line HL-60 from a promye
 R:Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdel, J.N.
 Science 228, 149-154, 1985
 A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
 A:Reference number: A44189; MUID:85142190; PMID:3856324
 A:Accession: A44189
 A:Molecule type: mRNA
 A:Residues: 1-62, 'S', 64-233 <WAN>

A>Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and A/Reference number: A61478; MUID:88301617; PMID:2841543
A/Accession: A61478
A/Molecule type: Protein
A/Residues: 56-79; 86-95, 'X', 97, 'X', 99; 119-151, 'XX', 154-162, 'X', 164, 'X', 166, 'X', 168, 'X', 170
R/Vogt, C.G.; Maurer-Fogy, I.; Adolf, G.R.
FEBS Lett. 314, 85-88, 1992
A/Title: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosylation
A/Reference number: S26951; MUID:93083656; PMID:1451807
A/Accession: S26951
A/Molecule type: protein
A/Residues: 35-59, N', 61-205 <VOI>
A/Note: 60-thr was also found
R/Fukushima, K.; Watanabe, H.; Takeo, K.; Nomura, M.; Asahi, T.; Yamashita, K.
Arch. Biochem. Biophys. 304, 144-153, 1993
A/Title: N-linked sugar chain structure of recombinant human lymphotoxin produced by CHO
A/Reference number: S34742; MUID:93311995; PMID:8323280
A/Contents: annotation
A/Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after induction, while having no detrimental effect on normal cells. It can also act synergistically with A/Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of different activities but are produced by different cell types and have different induction kinetics
C/Genetics:
A/Gene: GDB:17A; LT; TNFB
A/Cross-references: GDB:120442; OMIM:153440
A/Map position: 6p21.3-6p21.3
A/Introns: 33/3; 69/1
A/Note: the first intron occurs before the initiator codon
C/Superfamily: tumor necrosis factor
C/Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lymphokine; macrophage
F1-34/Domain: signal sequence #status predicted <SIG>
F35-205/Product: lymphotoxin #status predicted <SIG>
F41/Binding site: carbohydrate (Thr) (covalent) #status experimental
F96/Binding site: carbohydrate (Asn) (covalent) #status experimental
Query Match 9.5%; Score 122; DB 1; Length 205;
Best Local Similarity 23.4%; Pred. No. 0.0043;
Matches 37; Conservative 29; Mismatches 72; Indels 20; Gaps 5;
QY 85 AAHTGTGRSNTLSPPSKNEKALGRKINSHESSRSGHSFLSNHLRNGELVTHEKGY 144
DB 64 AAHLIGDPSKQNSL-----LNRANTDRAFLQDGFSLNSLLVPTSGY 107
QY 145 YVYSQTYRFOEIKENTKQMYQYTKYTS-YPDFTLLMKSNRNSCWSKDAEYGLYS 203
DB 108 FVYSQVVFSGKAYSPKATSSPLYLAEVQLFSSQYFFHVPDL-SSQKMYVQLQEPWLHS 166
QY 204 IVGGIFELKENDRIFVSVTN-EHLIDMDHEASPFQAF 240
DB 167 MYHGAFAQLTQGDQLSTHTDGIPLV-LSPSTVFFGAF 203
RESULT 9
OWNSN
tumor necrosis factor alpha precursor - mouse
N/Alternate names: cachectin; TNF alpha
C/Species: Mus musculus (house mouse)
C/Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 04-Feb-2000
C/Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696
R/Shitai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
DNA 7, 193-201, 1988
A/Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis
A/Reference number: A22908; MUID:88224564; PMID:2836146
A/Accession: A22908
A/Molecule type: DNA
A/Residues: 1-235 <SHI>
A/Cross-references: GB:M20155
R/Shakhov, A.N.; Nedospasov, S.A.
Bioorg. Khim. 13, 701-705, 1987
A/Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucle
A/Reference number: S03791; MUID:87298639; PMID:3040015
A/Accession: S03791
A/Molecule type: DNA

A/Residues: 1-235 <SHA>
A/Cross-references: GB:M38296; NID:G202086; PIDN:AAA40459.1; PID:G202087
A/Note: article in Russian with English abstract
R/Semon, D.; Kawashima, E.; Congenel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A/Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-tumor n
A/Reference number: A93679; MUID:88067722; PMID:3684584
A/Accession: A27303
A/Molecule type: DNA
A/Residues: 1-235 <SEM>
A/Cross-references: GB:Y00467; NID:G54830; PIDN:CAA68530.1; PID:G54832
R/Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985
A/Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necro
A/Reference number: A25164; MUID:85298296; PMID:3898078
A/Accession: A25164
A/Molecule type: mRNA
A/Residues: 1-235 <PEN>
A/Cross-references: GB:M11731; NID:G202084; PIDN:AAA40459.1; PID:G202085
R/Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashima
Nucleic Acids Res. 13, 4417-4429, 1985
A/Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic exp
A/Reference number: A23127; MUID:85242112; PMID:2989794
A/Accession: A23127
A/Molecule type: mRNA
A/Residues: 1-235 <PRA>
A/Cross-references: GB:X02611; NID:G54844; PIDN:CAA26457.1; PID:G54845
R/Cseh, K.; Beutler, B.
J. Biol. Chem. 264, 16256-16260, 1989
A/Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide result
A/Reference number: A34251; MUID:89380231; PMID:277790
A/Accession: A34251
A/Molecule type: protein
A/Residues: 70-87 <CSE>
R/Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A/Title: Identification of a common nucleotide sequence in the 3'-untranslated region
A/Reference number: I59058; MUID:86149365; PMID:2419912
A/Accession: I59058
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: mRNA
A/Residues: 1-230, 'R', 232-235 <RES>
A/Cross-references: GB:M13049; NID:G202082; PIDN:AAA40457.1; PID:G202083
R/Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
A/Title: Characterization of high molecular weight glycosylated forms of murine tumor
A/Reference number: A36696; MUID:91097531; PMID:2268312
A/Accession: A36696
A/Molecule type: protein
A/Residues: 80-85, 'X', 87-99 <SHE>
C/Genetics:
A/Introns: 62/3; 81/1; 97/1
A/Note: the first intron occurs in the 5'-untranslated region
C/Superfamily: tumor necrosis factor
C/Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; me
F80-235/Product: tumor necrosis factor #status experimental <WAT>
F20/Binding site: myristate (lys) (covalent) #status predicted
F84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F148-179/Disulfide bonds: #status predicted
Query Match 9.4%; Score 121; DB 1; Length 235;
Best Local Similarity 23.1%; Pred. No. 0.0063;
Matches 43; Conservative 34; Mismatches 79; Indels 30; Gaps 8;
QY 67 EKQNISPLVRGPRQVAAHITGRSNTLSSP-----NSKNEKALGRKINSHESSR 120
DB 62 EKFPNGLPLI-----SSMAQTILRSSQSSSKPVAVVAVNHQVEQL-----EWLSQR 111
QY 121 SGHSFLSNHLRNGELVTHEKGYFYQSYFFQBEIKENTKQMYQYTKYTS-YPDFTLLMKSNRNSCWSKDAEYGLYS 179
DB 112 ANALLANGMDLKDNLVVPADGLVLYVSQVLFKQG-----GCPDYVLLTHTVSRFAISYQ 166

QY 180 DPILLMKSARNCSWCKDAEYG-----LYSIYQGIFELKENDRIFVSVTNEHLIDMDHE 233
Db 167 EKNVLLSAVSKSPC-PKDTPEGAELKWPYEPYILVGGVFLQEKGDQLSAEVNPVKYLDFAES 225
QY 234 AS-FFG 238
Db 226 GQVYFG 231

RESULT 10

QY0029
tumor necrosis factor alpha precursor - rat
N;Alternate names: cachectin; TNF alpha
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence revision 07-Jun-1990 #text_change 04-Feb-2000
C;Accession: J00029; JN0868; S21674
R;Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.
Agric. Biol. Chem. 53, 1733-1736, 1989
A;Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosis factor alpha
A;Reference number: J00029
A;Accession: J00029
A;Molecule type: DNA
A;Residues: 1-235 <SH1>
R;Kwon, J.; Chung, I.Y.; Benveniste, E.N.
Gene 132, 227-236, 1993
A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
A;Reference number: JN0868; MUID:94040766; PMID:8224868
A;Accession: JN0868
A;Molecule type: DNA
A;Residues: 1-235 <KW>
A;Cross-references: GB:100981; NID:9205253; PIDN:AAAL6275.1; PID:g205254
R;Battler, H.C.; Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker, K.
Biochem. Biophys. Res. Commun. 192, 271-281, 1992
A;Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vitro
A;Reference number: S21674; MUID:92329007; PMID:1627266
A;Accession: S21674
A;Molecule type: mRNA
A;Residues: 1-38, 'P', 40-162, 'T', 164-201, 'S', 203-235 <EST>
A;Cross-references: GB:X65339; GB:S40199; NID:9395370; PIDN:CAA47146.1; PID:g395370
C;Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin and
C;Genetics:
A;Gene: TNF-alpha
A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; membrane
F;80-235/Product: tumor necrosis factor #status predicted <Mat>
F;19,20/Binding site: myristate (lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148-179/Disulfide bonds: #status predicted

Query Match 9.4%; Score 121; DB 2; Length 235;
Best Local Similarity 23.0%; Pred. NO. 0.0063;
Matches 43; Conservative 35; Mismatches 79; Indels 30; Gaps 8;
QY 66 QEQQNISPVLVRGPRQVAHITGTRSNLTSSP-----NSRNEKALGRKINSWESS 119
Db 61 EEKFNGLPLI-----SSMAQTLLRSSQNSDRKPVAVHVAHQAEQL-----EWLSQ 110
QY 120 RSCHSFLNLHLENGELVTHEKGFYIYSQTYFRQEEIKENTKNDKQVYIKYT-SY 178
Db 111 RANALLANGNDKNDQNLVVPADGLYISQVLPKQG-----GCPDYVLLTHTVSRFAISY 165
QY 179 PDPILLMKSARNCSWCKDAEYG-----LYSIYQGIFELKENDRIFVSVTNEHLIDMDH 232
Db 166 QEKVSLLSAISKSPC-PKDTPEGAELKWPYEPYILVGGVFLQEKGDLLSAEVNPKYLDITE 224
QY 233 EAS-FFG 238
Db 225 GQVYFG 231

RESULT 11

S22052
tumor necrosis factor alpha precursor - baboon
C;Species: Papio sp. (baboon)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: S22052
R;Sanjanwala, M.; Edwards, A.
submitted to the EMBL Data Library, September 1991
A;Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
A;Reference number: S22052
A;Accession: S22052
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <SAN>
A;Cross-references: EMBL:X62141; NID:g38159; PIDN:CAA44068.1; PID:g38160
C;Genetics:
A;Introns: 62/3; 78/1; 94/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F;19,20/Binding site: myristate (lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;145-177/Disulfide bonds: #status predicted
Query Match 9.3%; Score 120; DB 1; Length 233;
Best Local Similarity 23.0%; Pred. NO. 0.0076;
Matches 43; Conservative 32; Mismatches 70; Indels 42; Gaps 8;
QY 80 GPQR-----VAAHITGTRSNLTSSPNSK-----NEKALGRKINSWESSRSGH 123
Db 57 GPQREPFKDPSSLISLAQA VRSSRT---PSDKPVAVHVAHQAEQL---QWLNRANA 111
QY 124 SFLSNLHLENGELVTHEKGFYIYSQTYFRQEEIKENTKNDKQVYIKYT-----S 177
Db 112 LLANGVELRDNQNLVVPSEGLYISQVLPKQG-----GCPSTHVLTTHTISRIVS 162
QY 178 YPDPILLMKSARNCSWCK-----DASYGLYISYQGGIFELKENDRIFVSVTNEHLIDMDH 232
Db 163 YQTKVNLSSAISKSPCQRETPEGAEKWPYEPYILVGGVFLQEKGDRLSAEINLPYLDFAE 222
QY 233 EAS-FFG 238
Db 223 GQVYFG 229
RESULT 12
QY0529
tumor necrosis factor alpha precursor - sheep
N;Alternate names: cachectin; TNF alpha
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
C;Accession: JH0529; S48118; S13114; S20661
R;Green, I.R.; Sargan, D.R.
Gene 109, 203-210, 1991
A;Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with
A;Reference number: JH0529; MUID:92112044; PMID:1765267
A;Accession: JH0529
A;Molecule type: mRNA
A;Residues: 1-234 <GRE>
A;Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406
A;Experimental source: alveolar macrophage
R;Nash, A.D.; Bachman, G.J.; Brandon, M.R.; Andrews, A.E.
Immunol. Cell Biol. 69, 273-283, 1991
A;Title: Molecular cloning, expression and characterization of ovine TNF-alpha.
A;Reference number: S48118; MUID:92155784; PMID:1786996
A;Accession: S48118
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-234 <NMS>
A;Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807
R;Young, A.J.; Hay, J.B.; Chan, J.Y.C.
Nucleic Acids Res. 18, 6723, 1990
A;Title: Primary structure of ovine tumor necrosis factor alpha cDNA.
A;Reference number: S13114; MUID:91067496; PMID:2251151
A;Accession: S13114

A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-62,64-234 <YOU>
A;Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404
A;Note: comparison with the introns of homologous sequences suggest that this is probably
C;Superfamily: tumor necrosis factor
C;Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lympho
F;1-77/Domain: propeptide #status predicted <PRO>
F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F;20/Binding site: myristate (Iys) (covalent) #status predicted
F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;96/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;146-178/Disulfide bonds: #status predicted

Query Match 9.1%; Score 117.5; DB 1; Length 234;
Best Local Similarity 23.0%; Pred. No. 0.013;
Matches 42; Conservative 30; Mismatches 78; Indels 33; Gaps 7;

Qy 80 GPQRVAAHITG---TRGRSNTL--SSPNKNEKALGRKINS-----WESSRSGHSFLS 127
Db 57 GPQREOSGAPSPNRPVLVQTLSASSQASNNKPVAHVANISAPGQLRWGDSYANALMAN 116
Qy 128 NLHURNGLVTHEKGFYIYSQYVFRPQEEIKENTKNDKQMVYIYKYT-----SYDPP 181
Db 117 GVLEKDNQLVPTDGLYIYSQVLF-----GHGCPSTPLFLTHITISRIAVSYQTK 167
Qy 182 ILLMKARNCSWK-----DAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEAS- 235
Db 168 VNILSAIKSPCHRTLEGAEAKPWEPYIYOGGVFQLEKGRDLSEINLPYLDYAESGVYFC 227
Qy 236 FFG 238
Db 228 YFG 230

RESULT 13
S06192
tumor necrosis factor alpha precursor - goat (fragment)
N;Alternate names: cachectin; TNF alpha
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 31-Jan-2000
C;Accession: S06192; S41867
R;Goldstein, I.M.; Henner, D.; Talhouk, A.
submitted to the EMBL Data Library, March 1989
A;Reference number: S06192
A;Accession: S06192
A;Molecule type: mRNA
A;Residues: 1-193 <GOL>
A;Cross-references: EMBL:X14828; NID:g992; PIDN:CAA32937.1; PID:g993
R;Rinestad, E.
submitted to the EMBL Data Library, January 1994
A;Reference number: S41867
A;Accession: S41867
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 36-38,'S',40-78,'A',80-88,'N',90-114,'O',116-123,'D',125-144,'G',145-173,'L'
A;Cross-references: EMBL:X77317; NID:g452607; PIDN:CAA54523.1; PID:g452608
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage; membrane protein
F;42/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;106-138/Disulfide bonds: #status predicted

Query Match 9.0%; Score 115.5; DB 2; Length 193;
Best Local Similarity 20.4%; Pred. No. 0.014;
Matches 45; Conservative 36; Mismatches 79; Indels 61; Gaps 9;

Qy 29 FNDEESMNSPCQVQKQQLRWKMLRSTSTVQEKQONTSPVLRERGPGQVAAHI 88
Db 19 PEEQSPAGPSFN-----RPLVQ--TLRSSQASS-----NKPVAHV 53
Qy 89 TGTGRSNTLSPPNSKNEKALGRKINSWESSRSGHSFLSNLHNRGLVTHEKGFYIYS 148
Db 54 VA-----NISAPGQLR-----WGDSYANALKANGVELKDNQLVPTDGLYIYS 97

Qy 149 QTYFRFOEIKENTKNDKQMVYIYKYT-----SYDPPILLMKARNCSWK-----DAE 198
Db 98 QVLF-----GHGCPSTPLFLTHITISRIAVSYQTKVNILSAIKSPCHRTPEAEAK 148
Qy 199 YGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEAS-FFG 238
Db 149 PWYEPYIYOGGVFQLEKGRDLSEINLPYLDYAESGVYFC 189

RESULT 14
B27303
tumor necrosis factor beta precursor - mouse
N;Alternate names: lymphotoxin; TNF beta
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 24-Sep-1999
C;Accession: B27303; S01342; S10083; I56004; I48853; I55980
R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor n
A;Reference number: A33679; MUID:88067722; PMID:3684584
A;Accession: B27303
A;Molecule type: DNA
A;Residues: 1-202 <SEM>
A;Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68529.1; PID:g54831
R;Nedospasov, S.A.; Hirt, B.; Shakhov, A.N.; Dobrynin, V.N.; Kawashima, E.; Accolla, R
Nucleic Acids Res. 14, 7713-7725, 1986
A;Title: The genes for tumor necrosis factor (TNF-alpha) and lymphotoxin (TNF-beta) ar
A;Reference number: S01342; MUID:87040736; PMID:3490653
A;Accession: S01342
A;Molecule type: DNA
A;Residues: 1-11;139-160,'CG',163-178 <NED>
A;Cross-references: EMBL:X06217
R;Weil, D.; Dautry, F.
Oncogene Res. 3, 409-414, 1988
A;Title: Induction of tumor necrosis factor-alpha and -beta and interferon-gamma mRNA
A;Reference number: S10083; MUID:89144562; PMID:3147435
A;Accession: S10083
A;Molecule type: mRNA
A;Residues: 6-202 <WEI>
A;Cross-references: EMBL:X14800; NID:g54833; PIDN:CAA32906.1; PID:g736269
R;Gardner, S.M.; Mock, B.A.; Hilgers, J.; Huppi, K.E.; Roeder, W.D.
J. Immunol. 139, 476-483, 1987
A;Title: Mouse lymphotoxin and tumor necrosis factor: Structural analysis of the clone
A;Reference number: I56004; MUID:87252204; PMID:2885372
A;Accession: I56004
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-25,'P',27-202 <RES>
A;Cross-references: GB:M17015; NID:gl98880; PIDN:AAA39450.1; PID:g387407
R;Gray, F.W.; Chen, E.; Li, C.B.; Tang, W.L.; Ruddle, N.
Nucleic Acids Res. 15, 3937, 1987
A;Title: The murine tumor necrosis factor-beta (lymphotoxin) gene sequence.
A;Reference number: I48853; MUID:87231097; PMID:3588316
A;Accession: I48853
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: DNA
A;Residues: 1-202 <RE2>
A;Cross-references: EMBL:X00137; NID:g54842; PIDN:CAA68330.1; PID:g54843
R;Li, C.
J. Immunol. 138, 4496-4501, 1987
A;Title: Cloning and expression of murine lymphotoxin cDNA.
A;Reference number: I55980; MUID:87224127; PMID:2884262
A;Accession: I55980
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-202 <RES>
A;Cross-references: GB:M16819; NID:g202088; PIDN:AAA40460.1; PID:g202089
C;Comment: The first intron occurs in the 5'-untranslated region.
C;Genetics:
A;Gene: Tnf
A;Map position: 17
A;Introns: 32/3; 66/1

Search completed: June 3, 2004, 09:04:57
Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2004, 08:57:01 ; Search time 17 Seconds
(without alignments)
744.297 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281

Perfect score: 1287

Sequence: 1 INELKQMDKYSGIACFL.....NEHLIDMDHEASPPGAPLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 56376

Minimum DB seq length: 0

Maximum DB seq length: 243

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	160	12.4	174	TN15_HUMAN	O95150 homo sapien
2	159.5	12.4	240	TN14_HUMAN	O43557 homo sapien
3	152.5	11.8	239	TN14_MOUSE	Q9qyh9 mus musculus
4	136.5	10.6	235	TNFB_RABIT	P04924 oryctolagus
5	134.5	10.5	204	TNFB_PIG	P26445 sus scrofa
6	132.5	10.3	234	TNFA_CAVPO	P51435 cavia porce
7	130	10.1	232	TNFA_PIG	P23563 sus scrofa
8	129.5	10.1	235	TNFA_PERLE	P36939 peromyscus
9	127.5	9.9	234	TNFB_BOVIN	Q06600 bos taurus
10	126	9.8	234	TNFA_HORSE	P29553 equus caball
11	125	9.7	233	TNFA_MARMO	O35734 marmota mon
12	123	9.6	233	TNFA_HUMAN	P01375 homo sapien
13	122.5	9.5	229	TNFA_CEREL	P51743 cervus elap
14	122	9.5	205	TNFB_HUMAN	P01374 homo sapien
15	122	9.5	232	TNFA_PANTR	Q8had9 pan troglod
16	121	9.4	235	TNFA_MOUSE	P06804 mus musculus
17	121	9.4	235	TNFA_RAT	P16599 rattus norv
18	120	9.3	205	TNFB_MARMO	Q9jmd9 marmota mon
19	120	9.3	233	TNFA_FAPSP	P33620 papio sp. (
20	118	9.2	233	TNFA_TURTR	Q9bea1 tursiops tr
21	117.5	9.1	201	TNFB_MACEU	Q9xt48 macropus eu
22	117.5	9.1	234	TNFA_SHEEP	P23383 ovis aries
23	117	9.1	233	TNFA_MACMU	P48094 macaca mula
24	117	9.1	233	TNFA_PAFHU	O77510 papio hamad
25	116.5	9.1	233	TNFA_CANFA	P51742 canis fami
26	116	9.0	233	TNFA_MACFA	P79337 macaca fasc
27	116	9.0	233	TNFA_SAISS	Q8mk98 salmieri sci
28	114	8.9	202	TNFB_MOUSE	P09425 mus musculus
29	113.5	8.8	233	TNFA_TRIVU	P79374 trichosurus
30	113.5	8.8	234	TNFA_BOVIN	P59684 bos indicus
31	113	8.8	233	TNFA_BOVIN	Q06599 bos taurus
32	113	8.8	233	TNFA_BUBBU	P59693 bubalus bub
33	113	8.8	233	TNFA_LAMGL	P59694 lama glama

ALIGNMENTS

RESULT 1

ID	TN15_HUMAN	STANDARD;	PRT;	174 AA.
AC	O95150;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor ligand superfamily member 15 (Vascular endothelial cell growth inhibitor) (TNF ligand-related molecule 1).			
GN	TNFSF15 OR VEGI OR TLI.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
[1]				
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Umbilical vein;			
RC	MEDLINE=99091541; PubMed=9872942;			
RA	Zhai Y., Ni J., Jiang G.-W., Lu J., Xing L., Lincoln C., Carter K.C.,			
RA	Janat F., Korzak D., Xu S., Rojas L., Aggarwal B.B., Ruben S.,			
RA	Li L.-F., Gentz R., Yu G.-L.,			
RT	"VEGI, a novel cytokine of the tumor necrosis factor family, is an angiogenesis inhibitor that suppresses the growth of colon carcinomas in vivo."			
RL	FASEB J. 13:181-189(1999).			
CC	- FUNCTION: Inhibits vascular endothelial growth and angiogenesis (in vitro).			
CC	- SUBUNIT: Homotrimer (Potential).			
CC	- SUBCELLULAR LOCATION: Type II membrane protein (Probable).			
CC	- TISSUE SPECIFICITY: Specifically expressed in endothelial cells. Detected in placenta, lung, kidney, skeletal muscle, pancreas, spleen, prostate, small intestine and colon.			
CC	- SIMILARITY: Belongs to the tumor necrosis factor family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; AF039330; AAD08783.1; -			
DR	HSSP; P50591; 1D0G.			
DR	Genew; HGNC:11931; TNFSF15.			
DR	MIM; 604052; -			
DR	GO; GO:0005887; C:integral to plasma membrane; TAS.			
DR	GO; GO:0005102; F:receptor binding; TAS.			
DR	GO; GO:0000074; P:regulation of cell cycle; TAS.			
DR	InterPro; IPR006053; TNF_abs.			
DR	InterPro; IPR006052; TNF_family.			
DR	InterPro; IPR008983; TNF_like.			
DR	InterPro; IPR003636; TNF_subf.			
DR	Pfam; PF00229; TNF; 1.			
DR	PRINTS; PR01234; TNFCROSISFCT.			
DR	ProDom; PD002012; TNF_subf; 1.			

P13296 capra hircu
Q8wnr1 delphinapte
Q06332 rattus norv
Q9b0m7 macaca neme
P59695 papio anubi
O77764 macropus eu
P10154 oryctolagus
Q9tav8 sus scrofa
P19101 felis silve
P56783 arabisopsia
Q32347 caulobacter
Q88w17 lactobacilli

34 112.5 8.7 234 1 TNFA_CAPHI
35 112 8.7 233 1 TNFA_DELLE
36 111.5 8.7 202 1 TNFB_RAT
37 111 8.6 240 1 TNFS_MACNE
38 110 8.5 233 1 TNFA_PAPAN
39 108 8.4 233 1 TNFA_MACEU
40 107 8.3 197 1 TNFB_RABIT
41 106.5 8.3 150 1 TNFC_PIG
42 104.5 8.1 233 1 TNFA_FELCA
43 77.5 6.0 229 1 CEMA_ARATH
44 75.5 5.9 142 1 KSAU_CAUCR
45 73.5 5.7 206 1 KGUA_LACPL

DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00049; TNF 2; 1.
KW Cytokine; Transmembrane; Glycoprotein; signal-anchor.
FT DOMAIN 1 12 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 13 25 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 26 174 EXTRACELLULAR (POTENTIAL).
FT DISULFID 85 125 POTENTIAL.
FT CARBOHYD 56 56 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 152 152 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 174 AA; 20131 MW; CCB83BA7E673B98 CRC64;
Query Match 12.4%; Score 160; DB 1; Length 174;
Best Local Similarity 35.3%; Pred. No. 2.5e-06;
Matches 49; Conservative 24; Mismatches 48; Indels 18; Gaps 8;
QY 116 WSSRSCHGFLN-LHLRNGELVIEHKGFIYYSQTYERFQ-----EIKENTKDK--QM 168
DB 42 WE-HEGLAFTKRMVYTNKFLIPSGDYFIYSQVTRFGMTSECEIRQAGRPKPSI 100
QY 169 VQYIKYT-SYDPILLMKASRNSCWSDAEVG---LYSIYGGIFELKENDRIFVSVTN 224
DB 101 TVVITKVTDSPEPTQLMGTKSVC-----EVGSNNWFQIYLGAMFSLQEGDKLMVNSD 155
QY 225 EHLIDMDHE-AGFFGAFLV 242
DB 156 ISLDVTKEDKTFFGAFL 174
RESULT 2
TN14_HUMAN STANDARD; PRT; 240 AA.
ID TN14_HUMAN Q9WV78; Q96LD2;
AC Q43557; Q75476; Q9WV78; Q96LD2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 14 (Herpesvirus entry
mediator-ligand) (HVEM-L).
GN TNFSF14 OR LIGHT OR HVEM-L.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=98122340; PubMed=9462508;
RA Mauri D.N., Ebner R., Montgomery R.I., Kochel K.D., Cheung T.C.,
RA Yu G.-L., Ruben S., Murphy M., Eisenberg R.J., Cohen G.H., Spear P.G.,
RA Ware C.F.;
RT "LIGHT, a new member of the TNF superfamily, and lymphotoxin alpha are
RT ligands for herpesvirus entry mediator.";
RL Immunity 8:21-30(1998).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Liver;
RX MEDLINE=9438532; PubMed=9765287;
RA Harrop J.A., McDonnell P.C., Brigham-Burke M., Lyn S.D., Minton J.,
RA Tan K.B., Dede K., Spanpanato J., Silverman C., Hensley P.,
RA Diprinzio R., Emery J.G., Deen K., Eichman C., Chabot-Fletcher M.,
RA Truneh A., Young P.R.;
RT "Herpesvirus entry mediator ligand (HVEM-L), a novel ligand for
RT HVEM/FR2, stimulates proliferation of T cells and inhibits HT29 cell
RT growth.";
RL J. Biol. Chem. 273:27548-27556(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND PROCESSING.
RX MEDLINE=21528948; PubMed=11673523;
RA Granger S.W., Butrovich K.D., Houshmand P., Edwards W.R., Ware C.F.;
RT "Genomic characterization of LIGHT reveals linkage to an immune
RT response locus on chromosome 19p13.3 and distinct isoforms generated
RT by alternate splicing or proteolysis.";
RL J. Immunol. 167:5122-5128(2001).
RN [4]

RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci R.P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Phaley J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Shailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Cytokine that binds to TNFRSF3/LTBR. Binding to the
CC decoy receptor TNFRSF6B modulates its effects. Activates NFkB,
CC stimulates the proliferation of T cells, and inhibits growth of
CC the adenocarcinoma HT-29. Acts as a receptor for Herpes simplex
CC virus.
CC -1- SUBUNIT: Homotrimer.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein and secreted
CC (isoform 1); Cytoplasmic (isoform 2).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O43557-1; Sequence=Displayed;
CC Name=2; Synonyms=LIGHT delta-TM;
CC IsoId=O43557-2; Sequence=VSP_006452;
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN THE SPLEEN BUT ALSO
CC FOUND IN THE BRAIN. WEAKLY EXPRESSED IN PERIPHERAL LYMPHOID
CC TISSUES AND IN HEART, PLACENTA, LIVER, LUNG, APPENDIX, AND KIDNEY,
CC AND NO EXPRESSION SEEN IN FETAL TISSUES, ENDOCRINE GLANDS, OR
CC NONHEMATOPOIETIC TUMOR LINES.
CC -1- INDUCTION: UPREGULATED AFTER T-CELL ACTIVATION.
CC -1- PTM: N-glycosylated.
CC -1- PTM: The soluble form of isoform 1 derives from the membrane form
CC by proteolytic processing.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -1- CAUTION: Ref.4 sequence differs from that shown due to a
CC frameshift in position 178.
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CC or send an email to license@isb-sib.ch).
CC EMBL; AF036581; AAC39563.1; -
DR EMBL; AF064090; AAC25169.1; -
DR EMBL; AY028261; AAK36160.1; -
DR EMBL; BC018058; AAH18058.1; ALT_FRAME.
DR HSSP; P01375; 4TSV.
DR Genew; HGNC:11930; TNFSF14.
DR MIM; 604520; -
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0006917; P:induction of apoptosis; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Fram; PF00229; TNF; 1.

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DR PRINTS; PRO1234; TNFNECROSISFCT.
DR ProDom; PD002012; TNF subf; 1.
DR SMART; SMO0207; TNF; 1.
DR PROSITE; PS00251; TNF_1; FALSE_NEG.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor;
KW Alternative splicing.
FT CHAIN 1 240
FT CHAIN 783 240
FT CHAIN 1 37
FT CHAIN 58
FT CHAIN 59 240
FT CHAIN 82 83
FT CHAIN 154 187
FT CHAIN 102 102
FT CHAIN 38 73
FT CHAIN 120 120
FT CHAIN 214 214
FT CHAIN 240 AA; 26351 MW; 49D0BF67E1390B39 CRC64;
SQ SEQUENCE 240 AA; 26351 MW; 49D0BF67E1390B39 CRC64;

Query Match 12.4%; Score 159.5; DB 1; Length 240;
Best Local Similarity 23.8%; Pred No. 4.2e-06;
Matches 53; Conservative 41; Mismatches 66; Indels 63; Gaps 9;

Qy 41 QYKWLQRLVRLKMLTBEETISTVQEKQON-ISPLVERGPQVVAHITGRSNTLS 99
Db 60 QLHWELGEMVTRLPDGPAGSWEQLIQERRSHEVNP-----AAHLTGANSLSLTGS 109
Qy 100 SPNSKXKALGRKINSWESSRSGHSLNHLRNGELVIHEKGYIYQYVFRQEEIK 159
Db 110 GP-----LLWE-TQLGLAFLRGLSHVDGALVVRKAGYIYYSK----- 146
Qy 160 ENTKNDKQVQY-----IYKYT-SYDPFILLMKSRNSCKDAEYGLY 202
Db 147 -----VOLGGVCPGLASTTTHGLYKTPRYPELELLVQSQPCGRATSSSRVW 197
Qy 203 --SIYQGFELKENDRIFVSVTNEHLDM-DHEASFFGAFV 242
Db 198 WDSFLGGVVHLEAGEEVVVRVLDRLRLRDLRGTSTRSYFGAFV 240

RESULT 3
ID TN14_MOUSE STANDARD; PRT; 239 AA.
AC Q9QYH9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Tumor necrosis factor ligand superfamily member 14.
GN TNFSF14 OR LIGHT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20155223; PubMed=10700230;
RA Tamada K., Shimozaki K., Chapoval A.I., Zhu G., Sica G., Flies D.,
RA Boone T., Heu H., Fu Y.-X., Nagata S., Ni J., Chen L.;
RA "Modulation of T-cell-mediated immunity in tumor and graft-versus-host
RT disease models through the LIGHT co-stimulatory pathway.";
RL Nat. Med. 6:283-289 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20354998; PubMed=10894944;
RA Misawa K., Nosaka T., Kojima T., Hirai M., Kitamura T.;
RA "Molecular cloning and characterization of a mouse homolog of human
RT TNFSF14, a member of the TNF superfamily.";

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CytoGenet. Cell Genet. 89:89-91 (2000).
[3]
SEQUENCE FROM N.A.
TISSUE=Lymphoma;
Force W.R. Todd P.K., Mikayama T.;
"Mouse LIGHT; molecular genetics, ligand binding and expression.";
Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: Cytokine that binds to TNFRSF3/LTBR. Binding to the
decoy receptor TNFRSF6B modulates its effects. Activates NFkB
and stimulates the proliferation of T cells.
-1- SUBUNIT: Homotrimer (By similarity).
-1- SUBCELLULAR LOCATION: Type II membrane protein and secreted (By
similarity).
-1- PTM: The soluble form derives from the membrane form by
proteolytic processing.
-1- SIMILARITY: Belongs to the tumor necrosis factor family.
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EMBL; AF123385; AAF76453.1; -.
EMBL; AB029155; BAA8559.1; -.
EMBL; AE227533; AAF36722.1; -.
HSP; P01375; trsv.
MGD; MGI:1355317; Tnfsl4.
InterPro; IPR006053; TNF abc.
InterPro; IPR006052; TNF family.
InterPro; IPR008983; TNF like.
InterPro; IPR003636; TNF_subf.
Pfam; PF00229; TNF; 1.
PRINTS; PR01234; TNFOSISFCT.
ProDom; PD002012; TNF subf; 1.
SMART; SMO0207; TNF; 1.
PROSITE; PS00251; TNF_1; FALSE_NEG.
PROSITE; PS00049; TNF_2; 1.
Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT CHAIN 1 239
FT CHAIN 782 239
FT CHAIN 1 37
FT CHAIN 38 58
FT CHAIN 59 239
FT CHAIN 81 82
FT CHAIN 152 187
FT CHAIN 100 100
FT CHAIN 191 191
FT CHAIN 239 AA; 26338 MW; 217874AC71AD6BE3 CRC64;
SQ SEQUENCE 239 AA; 26338 MW; 217874AC71AD6BE3 CRC64;

Query Match 11.8%; Score 152.5; DB 1; Length 239;
Best Local Similarity 29.2%; Pred. No. 1.6e-05;
Matches 47; Conservative 25; Mismatches 72; Indels 17; Gaps 6;

Qy 85 AAHITGRGRSNTLSSENKSKALGRKINSWESSRSGHSLNHLRNGELVIHEKGY 144
Db 93 AAHLTGANSLSLTGS-----LLWE-TQLGLAFLRGLSHVDGALVVRKAGY 139
Qy 145 YIYQYVFRQEEIKENTKNDKQVYIYKTS-YDPFILLMKSRNSCKDAEYGLY- 202
Db 140 YVYSKVQLS-GVGCPCQGLANGLPITHGLYKTRYPKELELLVRRSPCGRANSRVWD 198
Qy 203 SIYQGFELKENDRIFVSVTNEHLI-DMDHEASFFGAFV 242
Db 199 SSFLGGVVHLEAGEEVVVRVPGNRLVPRDGTSTRSYFGAFV 239

RESULT 4

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TNFA_RABIT
ID TNFA_RABIT STANDARD; PRT; 235 AA.
AC P04924.
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91065534; PubMed=2249779;
RA Shakhov A.N., Kuprash D.V., Azizov M.M., Jongeneel C.V.,
RA Nedospasov S.A.;
RT "Structural analysis of the rabbit TNF locus, containing the genes
RT encoding TNF-beta (lymphotoxin) and TNF-alpha (tumor necrosis
RT factor).";
RL Gene 95:215-221(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86219712; PubMed=3519138;
RA Ito H., Shirai T., Yamamoto S., Akira M., Kawahara S., Todd C.W.,
RA Wallace R.B.;
RT "Molecular cloning of the gene encoding rabbit tumor necrosis
RT factor.";
RL DNA 5:157-165(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=86219711; PubMed=3519137;
RA Ito H., Yamamoto S., Kuroda S., Sakamoto H., Kajihara J., Kiyota T.,
RA Hayashi H., Kato M., Seko M.;
RT "Molecular cloning and expression in Escherichia coli of the cDNA
RT coding for rabbit tumor necrosis factor.";
RL DNA 5:149-156(1986).
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- DISEASE: Cachexia accompanies a variety of diseases, including
CC cancer and infection, and is characterized by general ill health
CC and malnutrition.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
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EMBL; M12845; AAA31486.1; --
EMBL; M12846; AAA31482.1; --
EMBL; M60340; AAA31484.1; --
PIR; A25454; A25451.
HSP; P06804; 2TNF.
InterPro; IPR006053; TNF_abc.

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DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS00049; TNF 2; 1.
DR Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
KW CYTOKINE; TRANSMEMBRANE; SIGNAL-ANCHOR; PHOSPHORYLATION.
FT CHAIN 1 235
FT CHAIN 80 235
FT DOMAIN 1 35
FT TRANSMEM 36 56
FT POTENTIAL.
FT DOMAIN 57 235
FT SITE 79 80
FT MOD_RES 2 2
FT DISULFID 148 179
FT CONFLICT 63
FT CONFLICT 235 AA; 25816 MW; 61017 DOB D2EF871 CRC64;
SQ SEQUENCE 235 AA; 25816 MW; 61017 DOB D2EF871 CRC64;

Query Match 10.6%; Score 136.5; DB 1; Length 235;
Best Local Similarity 23.0%; Pred. No. 0.00032;
Matches 42; Conservative 37; Mismatches 81; Indels 23; Gaps 7;

QY 72 ISPLVERGPQVAHITGRGSRNTL--SSPNSKNEKALGRKINS-----WESSRG 122
DB 56 IGCFEEQSPNNL--HLNFPVQMVTLRASRALSRLDKPLAHVAVNPQVSGQLWLSQRAN 113
QY 123 HSFLSNLHRLNGELVIHERGYYIYSQTYFRFQEEIKENTKNDKQMVQYIKY-TSPDP 181
DB 114 ALLANGKLTNDQLVVPADGLYLYSQVLFSQG-----GCRSYLLTHTVSRFAVSYPNK 168
QY 182 ILLMKASRNSCWSKDAEYG-----LYSIYQGIFELKENDRLFVSVTNEHLMDHEAS- 235
DB 169 VNLSIAIKSPCHRETPPEEAFPMWYEPYILGVGVFQLEKGRDUSTEVNQPEYLDLAESGV 228
QY 236 FFG 238
DB 229 YFG 231

RESULT 5
TNFB_PIG STANDARD; PRT; 204 AA.
ID TNFB_PIG STANDARD; PRT; 204 AA.
AC P26445;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lymphotoxin-alpha precursor (lir-alpha) (TNF-beta) (Tumor necrosis
DE factor ligand superfamily member 1).
GN LTA OR TNFSF1 OR TNFB.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91340150; PubMed=1874444;
RA Kuhnert P., Wuehrich C., Peterhans E., Pauli U.;
RT "The porcine tumor necrosis factor-encoding genes: sequence and
RT comparative analysis."
RL Gene 102:171-178(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Large white; TISSUE=Fibroblast;
RX MEDLINE=21108615; PubMed=11169259;
RA Chardon P., Rogel-Gaillard C., Cattolico L., Duprat S., Vaiman M.,
RA Renard C.;
RT "Sequence of the swine major histocompatibility complex region
RT containing all non-classical class I genes."

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RL Tissue Antigens 57:55-65(2001).
CC -!- FUNCTION: Cytokine that in its homotrimeric form binds to
CC TNFRSF1A/TNFR1, TNFRSF1B/TNFR and TNFRSF14/HVEM. In its
CC heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
CC produced by lymphocytes and cytotoxic for a wide range of tumor
CC cells in vitro and in vivo.
CC -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC LTA subunits or (less prevalent) two LTA and one LTB subunits (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC associated (heterotrimers) (By similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC
CC EMBL; X54859; CAA38638.1; -.
CC EMBL; AJ251914; CAB63853.1; -.
CC PIR; S17289; S17289.
CC HSSP; P01374; 1TNR.
CC InterPro; IPR006053; TNF abc.
CC InterPro; IPR006052; TNF_family.
CC InterPro; IPR008983; TNF_like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01234; TNECROSISFCT.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS0049; TNF_2; 1.
CC Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 33
FT CHAIN 34 204 LYMPHOTOXIN-ALPHA.
FT CARBOHYD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 204 AA; 21960 MW; 812633187435856AC CRC64;

Query Match 10.5%; Score 134.5; DB 1; Length 204;
Best Local Similarity 24.7%; Pred. No. 0.00039;
Matches 46; Conservative 31; Mismatches 76; Indels 33; Gaps 7;

QY 63 STVQKQNIQPLVREGRQVAAHITG-----TGRSNTLSGPSNKKKALGRKINS 115
DB 42 SAAQPAHQH-PPKHLARTGLKPAHLVGDPTPSLRWANT-----DRAFLR---- 88

QY 116 WESSRSGHSFLSNLHRLNGELVIHEKGYIYYSQTYFRFQBEIKENTKNDKQVQYIYKY 175
DB 89 -----HGFL-----LSNNLLIVPTSGLYFVYSQVVSFGCGFPKATPTPLYLAHEVQLF 137

QY 176 TS-YDPDILLMKARSNCWSKDAEYGLYSIVGGGIFELKENDRIFVSVTNEHLIDMDHEA 234
DB 138 SSQYFFHPLLSAQSKVCPGPGPW-VRSVYQGVAFLLTQGDQSTHTDGTPHLLSPSS 196

QY 235 SFFGAF 240
DB 197 VFFGAF 202

RESULT 6
TNFA_CAVPO STANDARD; PRT; 234 AA.
AC P51435;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1995 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
GN TNF OR TNFSF2 OR TNFA.
OS Cavia porcellus (Guinea pig).

```

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hartley; TISSUE=Lung;
RA Yuan H.T., Kelly F.J., Single C.D.;
RT "Cloning and characterization of guinea pig TNF-alpha cDNA.";
RN Submitted (NOV-1995) to the EMBL/GenBank/DBSJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Dunkin-Hartley;
RX MEDLINE=97462215; PubMed=9316485;
RA White A.W., Yoshimura T., Smith A.W., Westwick J., Watson M.L.;
RT "Airway inflammation induced by recombinant guinea pig tumor necrosis
RT factor-alpha.";
RL Am. J. Physiol. 273:L524-L530(1997).
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- DISEASE: Cachexia accompanies a variety of diseases, including
CC cancer and infection, and is characterized by general ill health
CC and malnutrition.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U39839; AAB06492.1; -.
CC EMBL; U77036; AAB19210.1; -.
CC HSSP; P06804; 2TNF.
CC InterPro; IPR006053; TNF_abc.
CC InterPro; IPR006052; TNF_family.
CC InterPro; IPR008983; TNF_like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF; 1.
CC PRINTS; PR01234; TNECROSISFCT.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS0049; TNF_2; 1.
CC Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT CHAIN 1 234 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 80 234 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 57 234 EXTRACELLULAR (POTENTIAL).
FT SITE 79 80 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT DISULFID 147 178 BY SIMILARITY.
SQ SEQUENCE 234 AA; 25793 MW; 7272C940393E7E9B CRC64;

Query Match 10.3%; Score 132.5; DB 1; Length 234;
Best Local Similarity 24.6%; Pred. No. 0.00068;

```

	Matches	44; Conservative	33; Mismatches	77; Indels	25; Gaps	7;
Qy	80	GPORVAAHIIGT--RGESNTL-----SSPNSKNEKALGRKINS-----WESSRSGHSFL	126			
Db	57	GPQEEQFSGPFRPLAQTLTIRASQNDKFAHVANQAEEELQHLSKRANALLA	116			
Qy	127	SNLHLRNGELVIVHEKGFYYIYQTYFRFBEIKENTKNDKMQVQIYKY-TSYPDPIILM	185			
Db	117	NGMGLSDNLVWPDSGLYIYQVLFGQ-----GCPSYLLLTHTVSRLAIVPEKVNLL	171			
Qy	186	KSARNSCWSKDAEYV-----LYSYIQGIGITELKENDRIFVSVTNEHLIDM-DHEASPFQ	238			
Db	172	SAIKSPCKQETPEGAERKPMVEPYLGGVQLQKGRLSAEVNLFOYLDPADSQIYFG	230			

RESULT 7	TNFA_PIG	TNFA_PIG	STANDARD;	PRT;	232 AA.
ID	TNFA_PIG	TNFA_PIG	STANDARD;	PRT;	232 AA.
AC	P23563;				
DT	01-NOV-1991 (Rel. 20, Created)				
DT	01-NOV-1991 (Rel. 20, Last sequence update)				
DT	10-OCT-2003 (Rel. 42, Last annotation update)				
DE	Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor				
DE	ligand superfamily member 2) (TNF-a) (Cachectin).				
GN	TNF OR TNFSF2 OR TNFA.				
OS	Sus scrofa (Pig).				
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.				
OX	NCBI_TaxID=9823;				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=91016861; PubMed=2216741;				
RX	Drews R.T., Coffee B.W., Prestwood A.K., McGraw R.A.;				
RT	"Gene sequence of porcine tumor necrosis factor alpha.";				
RL	Nucleic Acids Res. 18:5564-5564(1990).				
RL	[2]				
RC	SEQUENCE FROM N.A.				
RC	TISSUE=Liver;				
RK	MEDLINE=91340150; PubMed=1874444;				
RT	Kuhnert P., Wuethrich C., Peterhans E., Pauli U.;				
RL	"The porcine tumor necrosis factor-encoding genes: sequence and				
RL	comparative analysis.";				
RL	Gene 102:171-178(1991).				
RL	[3]				
RP	SEQUENCE FROM N.A.				
RP	TISSUE=Macrophage;				
RC	Choi C.S., Molitor T.W., Lin G.F., Murtaugh M.P.;				
RT	"Complete nucleotide sequence of a cDNA encoding porcine tumor				
RL	necrosis factor-alpha.";				
RL	Anim. Biotechnol. 2:97-105(1991).				
RL	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=large white; TISSUE=Fibroblast;				
RK	MEDLINE=21108615; PubMed=11169259;				
RT	Chardon P., Rogei-Galliard C., Cattolico L., Duprat S., Vaiman M.;				
RL	Renard C.;				
RT	"Sequence of the swine major histocompatibility complex region				
RL	containing all non-classical class I genes.";				
RL	Tissue Antigens 57:55-65(2001).				
RL	[5]				
RP	SEQUENCE OF 44-232 FROM N.A.				
RK	MEDLINE=90034181; PubMed=2478420;				
RT	Pauli U., Beutler B., Peterhans E.;				
RL	"Porcine tumor necrosis factor alpha: cloning with the polymerase				
RL	chain reaction and determination of the nucleotide sequence.";				
RL	Gene 81:185-191(1989).				
CC	-I- FUNCTION: Cytokine that binds to TNFSF1A/TNFR1 and				
CC	induces cell death of certain tumor cell lines. It is potent				
CC	pyrogen causing fever by direct action or by stimulation of				
CC	interleukin 1 secretion and is implicated in the induction of				
CC	cachexia. Under certain conditions it can stimulate cell				
CC	proliferation and induce cell differentiation.				

```

CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- DISEASE: Cachexia accompanies a variety of diseases, including
CC cancer and infection, and is characterized by general ill health
CC and malnutrition.
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
-----
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-----
CC EMBL; X54001; CAA37949.1; -
CC EMBL; X54859; CAA38639.1; -
CC EMBL; X57321; CAA40591.1; -
CC EMBL; AJ251914; CAB63852.1; -
CC EMBL; M29079; AAA11128.1; -
CC EMBL; PIR; S12606; S12606.
CC HSSP; P01375; 4TSV.
CC InterPro; IPR006053; TNF abc.
CC InterPro; IPR006052; TNF family.
CC InterPro; IPR008983; TNF like.
CC InterPro; IPR003636; TNF_subf.
CC Pfam; PF00229; TNF_1.
CC PRINTS; PR01234; TNECROSISPT.
CC ProDom; PD002012; TNF_subf; 1.
CC SMART; SM00207; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS00049; TNF_2; 1.
CC Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
CC CHAIN 1 232 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
CC FT CHAIN 77 232 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
CC FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT FT FT (POTENTIAL).
CC FT DOMAIN 57 232 EXTRACELLULAR (POTENTIAL).
CC FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
CC FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
CC FT DISULFID 144 176 BY SIMILARITY.
CC FT SEQUENCE 232 AA; 25254 MW; 65B28F702D99C8BE CRC64;
-----
Query Match 10.1%; Score 130; DB 1; Length 232;
Best Local Similarity 25.1%; Pred. No. 0.0011;
Matches 43; Conservative 30; Mismatches 78; Indels 20; Gaps 6;
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QY 80 GPORVAHITGTRGNLTLSPPNS---XNEKALGRKINSWESSRSGHSFLSNLHRLNGEL 136
DB 66 GPLSINPLAQLRSSQTSQDKPVAVHVANVKAEGQL--QWQSGVANALLANGVKLKDQNL 123
-----
QY 137 VIHEKGFVYYSQTYRPFQEEIKEN---TKNDQKVQYIYKYTSYDPDILLMKSARNCSW 193
DB 124 VPTDGLYLYISQVLFRGQCPTNVLHTTISRIA-----VSYQTKVLLSAIKSPQC 177
-----
QY 194 SK-----DABEGLYSIQGGIFELKENDRIFVSTNEHLIDMDHEAS-FFG 238
DB 178 RETPEGAEKPWVEPIYLGGVFQLEKDDRLSAEINLPDYLDFAESGQVYFG 228
-----
RESULT 8
TNFA_PERLE STANDARD; PRT; 235 AA.
ID TNFA_PERLE AC P36939;
DT 01-JUN-1994 (Rel. 29, Created)

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01-JUN-1994 (Rel. 29, Last sequence update)
 10-OCT-2003 (Rel. 42, Last annotation update)
 Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 ligand superfamily member 2) (TNF-a) (Cachectin).
 TNF OR TNFSF2 OR TNFA.
 Peromyscus leucopus (White-footed mouse).
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
 Peromyscus.
 NCBI_TaxID=10041;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=92218012; PubMed=1348497;
 Crew M.D., Filipowicz M.E.;
 "Sequence of the tumor necrosis factor/cachectin (TNF) gene from
 Peromyscus leucopus (family Cricetidae).";
 Immunogenetics 35:351-353(1992).
 -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 induce cell death of certain tumor cell lines. It is potent
 pyrogen causing fever by direct action or by stimulation of
 interleukin 1 secretion and is implicated in the induction of
 cachexia. Under certain conditions it can stimulate cell
 proliferation and induce cell differentiation.
 -!- SUBUNIT: Homotrimer (By similarity).
 -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 extracellular soluble form (By similarity).
 -!- PM: The soluble form derives from the membrane form by
 proteolytic processing (By similarity).
 -!- PM: The membrane form, but not the soluble form, is
 phosphorylated on serine residues. Dephosphorylation of the
 membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 similarity).
 -!- DISEASE: Cachexia accompanies a variety of diseases, including
 cancer and infection, and is characterized by general ill health
 and malnutrition.
 -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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 EMBL; M59233; AAA40596.1; --
 PIR; I54490; I54490.
 HSP; P06804; 2TNF.
 InterPro; IPR006053; TNF-abc.
 InterPro; IPR006052; TNF family.
 InterPro; IPR008983; TNF-like.
 InterPro; IPR003636; TNF_subf.
 Pfam; PF00229; TNF; 1
 PRINTS; PR01234; TNCRSISFCT.
 ProDom; PD002012; TNF_subf; 1.
 DR PROSITE; PS00251; TNF 1; 1.
 DR PROSITE; PS0049; TNF 2; 1.
 KW Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
 FT CHAIN 1 235 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
 FT DOMAIN 80 235 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
 FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 (POTENTIAL).
 FT DOMAIN 57 235 EXTRACELLULAR (POTENTIAL).
 FT SITE 79 80 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
 FT MOD RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
 FT DISULFD 148 179 BY SIMILARITY.
 FT CARBOHYD 86 86 N-LINKED (GLCNAC...) (POTENTIAL).
 SQ SEQUENCE 235 AA; 25822 MW; 235ASCF9F9AC624 CRC64;
 Query Match 10.1%; Score 129.5; DB 1; Length 235;

Best Local Similarity 24.5%; Pred. No. 0.0012;
 Matches 45; Conservative 39; Mismatches 75; Indels 25; Gaps 9;
 QY 72 ISPLVREGQORVAHITGTGRSNTL-SSPNSKNEKALGRKINSWE-----SSRSQH 123
 DB 56 IGPOREKFPNNLP--IIGSMAQTLLRSSQNSDKPVAHVAVNHQVDEQLWLSRGN 113
 QY 124 SFLSN-LHLRNGELVIEHKGFIYISQTYFRQBEIKENTKNDKQMYQYIKY-TSYDP 181
 DB 114 ALLANGMDLKNQVLIPADGLVLYVSQVLFKQ-----GCSSYVLLTHTVSRAVSYEDK 168
 QY 182 ILLMKSARNCSWSDAAYG-----LYSIYOGGFFELKENDRIFFSVTNEHLIMDHEAS 235
 DB 169 VNLISAIRKSPC-PRKTEPGESELKPWFYFIYLGGVFQLEKGRDLSEAVNLPKYLDFASGQ 227
 QY 236 -FFG 238
 DB 228 VYFG 231
 RESULT 9
 TNFB BOVIN
 ID TNFB BOVIN STANDARD; PRT; 204 AA.
 AC Q06600;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
 factor ligand superfamily member 1).
 GN LTA OR TNFSF1 OR TNFB.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94083525; PubMed=8260599;
 RA Cludes I., Cluter Y., Kettmann R., Burny A., Droogmans L.;
 "Cloning and characterization of the tandemly arranged bovine
 Lymphotoxin and tumour necrosis factor-alpha genes.";
 RT Cytokine 5:338-341(1993).
 RL Cytokine 5:338-341(1993).
 CC -!- FUNCTION: Cytokine that in its homotrimeric form binds to
 TNFRSF1A/TNFR1, TNFRSF1B/TNFR and TNFRSF14/HVEM. In its
 heterotrimeric form with LTB binds to TNFRSF3/LTBR. Lymphotoxin is
 produced by lymphocytes and cytotoxic for a wide range of tumor
 cells in vitro and in vivo.
 CC -!- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
 LTA subunits or (less prevalent) two LTA and one LTB subunits (By
 similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
 associated (heterotrimers) (By similarity).
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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 EMBL; Z14137; CA478510.1; --
 DR PIR; I46046; S24641.
 DR HSP; P01374; 1TNR.
 DR InterPro; IPR006053; TNF-abc.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF-like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01234; TNCRSISFCT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.

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DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS0049; TNF 2; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 33
FT CHAIN 34 204
FT CARBOHYD 95
SQ SEQUENCE 204 AA; 22098 MW; 52A9F0A2CEDB5425 CRC64;

Query Match 9.9%; Score 127.5; DB 1; Length 204;
Best Local Similarity 24.9%; Pred. No. 0.0015;
Matches 47; Conservative 29; Mismatches 78; Indels 35; Gaps 9;

QY 61 TISIVQEQKQMSILVBERGQORVAHITG-----TRGSNTLSPNKNKALGRKI 113
DB 40 TPSAAQPAHQQL-PTPFRGTGLKFAAHLVGPDPSTQDSLWRANT-----DRAFLR-- 88
QY 114 NSWESSRSGHGSFLNLHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVYIY 173
DB 89 -----HGF-----SLNNLSLVPTSLGLYFVVSQVFSGRGCFPRATPTPLYLAHEVQ 135
QY 174 KYT-SYDPDILIMKSNKSWKDAEYGLIYSIQGGIFELKENDRIFVSVTN-EHLIDMD 231
DB 136 LFSQYPPFHVFLLSAQSKVCPGQGPW-VRSVYQGAPELLTRGDQLSTHTDGTSHLL-LS 193
QY 232 HEASPFAGF 240
DB 194 PSSVFFGAF 202

RESULT 10
ID TNFA HORSE STANDARD; PRT; 234 AA.
AC P29553; Q9PTJ3;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=92084125; PubMed=1748301;
RX Su X., Morris D.D., McGraw R.A.;
RT "Cloning and characterization of gene TNF alpha encoding equine tumor
RT necrosis factor alpha."
RL Gene 107:319-321(1991).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=Thoroughbred; TISSUE=Artery;
RA Ishida N., Sato F., Hasegawa T.;
RT "Molecular cloning of equine tumor necrosis factor-alpha mRNA."
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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CC -----
DR EMBL; M64087; AAA30959.1; -.
DR EMBL; AB035735; BAA88349.1; -.
DR PIR; J01344; J01344.
DR HSP; P01375; IABM.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF-like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PRO1234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS0049; TNF 2; 1.
KW Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT CHAIN 1 234
FT CHAIN 78 234
FT DOMAIN 1 35
FT TRANSMEM 36 56
FT DOMAIN 57 234
FT SITE 77 78
FT MOD RES 2 2
FT DISULFID 146 178
FT CONFLICT 177 179
FT SEQUENCE 234 AA; 25469 MW; E79ACE91143DF373 CRC64;
SQ
Query Match 9.8%; Score 126; DB 1; Length 234;
Best Local Similarity 22.5%; Pred. No. 0.0023;
Matches 45; Conservative 35; Mismatches 72; Indels 48; Gaps 9;

QY 62 ISTVQEQK-----QNISPLVR-----ERGF-QRVAHITGTRGRNTLSPNKNKALG 110
DB 56 IGPQREQLPNAPQSINPLAQLTRSSSRTPSDKPAHVVA-----NPAERG 101
QY 111 RKNWESSRSGHGSFLNLHLRNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQ 170
DB 102 QL--QWLGRANALLANGVKLTDNLVPLDGLIYISQVLFKQ-----GCPSTH 150
QY 171 YIVKYT-----SYDPDILIMKSNKSWKDAEYG-----LYSIYQGGIFELKENDRIF 219
DB 151 VLLHTISRLAVSPKSNKLLSAIKSPCHTESPEQAEAKPWYEPYILGGVFLQEKGDQLS 210
QY 220 VSVTNEHLIDMDHEAS-FFG 238
DB 211 AEINQPNYLDFAESGQVYFG 230

RESULT 11
ID TNFA MARMO STANDARD; PRT; 233 AA.
AC O35734;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]

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SEQUENCE FROM N.A.
 RC TISSUE=Peripheral blood;
 RX MEDLINE=98139533; PubMed=9472070;
 RA Lohrengel B., Lu M., Roggendorf M.;
 RT "Molecular cloning of the woodchuck cytokines: TNF-alpha, IFN-gamma,
 and IL-6";
 RL Immunogenetics 47:332-335 (1998).
 [2]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Peripheral blood;
 RA Zhou H., Hu J., Seeger C.;
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 [3]
 RC SEQUENCE FROM N.A.
 RC TISSUE=Peripheral blood;
 RX MEDLINE=20184746; PubMed=10721723;
 RA Li D.H., Havell E.A., Brown C.L., Cullen J.M.;
 RT "Woodchuck lymphotxin-alpha, -beta and tumor necrosis factor genes:
 structure, characterization and biological activity";
 RL Gene 242:295-305 (2000).
 [4]
 RC SEQUENCE FROM N.A.
 RA Hodgson P.D., Michalak T.I.;
 RT "Augmented hepatic interferon gamma expression and T cell influx
 characterize acute hepatitis progressing to recovery and residual
 lifelong virus persistence in experimental adult woodchuck hepatitis
 virus infection";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can
 induce cell death of certain tumor cell lines. It is potent
 pyrogen causing fever by direct action or by stimulation of
 interleukin 1 secretion and is implicated in the induction of
 cachexia. Under certain conditions it can stimulate cell
 proliferation and induce cell differentiation.
 CC -!- SUBUNIT: Homotrimer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 extracellular soluble form (By similarity).
 CC -!- PMW: The soluble form derives from the membrane form by
 proteolytic processing (By similarity).
 CC -!- PTM: The membrane form, but not the soluble form, is
 phosphorylated on serine residues. Dephosphorylation of the
 membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 similarity).
 CC -!- DISEASE: Cachexia accompanies a variety of diseases, including
 cancer and infection, and is characterized by general ill health
 and malnutrition.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.

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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

 DR EMBL; Y14137; CAA74569.1; -;
 DR EMBL; AF082491; AAC32615.1; -;
 DR EMBL; AF012910; AAF34863.1; -;
 DR EMBL; AF095268; AAF34867.1; -;
 DR EMBL; AF333967; AAK52718.1; -;
 DR HSSP; P06804; 2TNF.
 DR InterPro; IPR006053; TNF abc.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01234; TNFCROISFCT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF 1; 1.
 DR PROSITE; PS0049; TNF_2; 1.

KW Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
 FT CHAIN 1 233
 FT CHAIN 78 233
 FT DOMAIN 1 35
 FT TRANSMEM 36 56
 FT DOMAIN 57 233
 FT SITE 77 78
 FT MOD_RES 2 2
 FT DISULFID 146 177
 SQ SEQUENCE 233 AA; 25764 MW; 34D3D1965DAAE0E7 CRC64;
 Query Match 9.7%; Score 125; DB 1; Length 233;
 Best Local Similarity 23.2%; Pred. No. 0.0028;
 Matches 36; Conservative 30; Mismatches 69; Indels 20; Gaps 5;
 QY 99 SPSPKNEKALGRKINS-----WSSSRGHSFLSNLHUNGELVHEKGFYIYSQT 150
 DB 80 SSSQNMNDKPAHVAVAKNDEQLVLSRRANALLANGMELIDNQLVVPANGLYLVISQV 139
 QY 151 YFRFQEEIKENTKQNVQIYKY-TSPDPILLMKSAKNSCKSKDAEYGLYS-----I 204
 DB 140 LFRGQ-----GCPSYLLVTHVSRFAVYQDKVLLSAIKSPCKESLEGAEFKWYEP 194
 QY 205 YOGGIFELKENDRIEVSVTNEHLIDMDHEAS-FFG 238
 DB 195 YLGGVFEIQLKGRLSAEVNLPSYLDFAESGQVYFG 229
 RESULT 12
 TNFA_HUMAN STANDARD; PRT; 233 AA.
 ID P01375; O43647; Q9P1Q2; Q9UIV3;
 AC 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 ligand superfamily member 2) (TNF-a) (Cachectin).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_Taxid:9606;
 [1]
 RC SEQUENCE FROM N.A.
 RX MEDLINE=87217060; PubMed=3555974;
 RA Nedospasov S.A., Shakhov A.N., Turetskaya R.L., Mett V.A.,
 Azizov M.M., Georgiev G.P., Korobko V.G., Dobrynin V.N.,
 Philippov S.A., Bystrov N.S., Boldyreva E.F., Chuvpilo S.A.,
 Chumakov A.M., Shingarova L.N., Orzhinnikov Y.A.;
 RT "Random arrangement of genes coding for tumor necrosis factor (TNF-
 alpha) and lymphotoxin (TNF-beta) in the human genome";
 RL Cold Spring Harb. Symp. Quant. Biol. 51:611-624 (1986).
 [2]
 RC SEQUENCE FROM N.A.
 RX MEDLINE=85086244; PubMed=6392892;
 RA Pennica D., Nedwin G.E., Hayflick J.S., Seeburg P.H., Derynck R.,
 Palladino M.A., Kohr W.J., Aggarwal B.B., Goeddel D.V.;
 RT "Human tumour necrosis factor: precursor structure, expression and
 homology to lymphotoxin";
 RL Nature 312:724-729 (1984).
 [3]
 RC SEQUENCE FROM N.A.
 RX MEDLINE=85137898; PubMed=3883195;
 RA Shirai T., Yamaguchi H., Ito H., Todd C.W., Wallace R.B.;
 RT "Cloning and expression in Escherichia coli of the gene for human
 tumour necrosis factor";
 RL Nature 313:803-806 (1985).
 [4]
 RC SEQUENCE FROM N.A.
 RX MEDLINE=86016093; PubMed=2995927;
 RA Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D.H.,
 Jarrett-Nedwin J., Pennica D., Goeddel D.V., Gray P.W.;

RT "Human lymphotoxin and tumor necrosis factor genes: structure,
 RL homology and chromosomal localization.",
 RN Nucleic Acids Res. 13:6361-6373(1985).
 RP
 RX SEQUENCE FROM N.A.
 RA MEDLINE=95142190; PubMed=3856324;
 RA Wang A.M., Creasey A.A., Ladner M.B., Lin L.S., Strickler J.,
 RA von Arsdel J.N., Yamamoto R., Mark D.F.;
 RT "Molecular cloning of the complementary DNA for human tumor necrosis
 RT factor.",
 RL Science 228:149-154(1985).
 RN
 RP SEQUENCE FROM N.A.
 RA MEDLINE=86030296; PubMed=3932069;
 RA Marxenout A., Fransen L., Tavernier J., van der Heyden J., Tizard R.,
 RA Kawashima E., Shaw A., Johnson M.J., Senon D., Mueller R.,
 RA Ruysschaert M.R., van Vliet A., Piers W.;
 RT "Molecular cloning and expression of human tumor necrosis factor and
 RT comparison with mouse tumor necrosis factor.",
 RL Eur. J. Biochem. 152:515-522(1985).
 RN
 RP SEQUENCE FROM N.A.
 RA MEDLINE=93272029; PubMed=8499947;
 RA Iris F.J.M., Bougueleret L., Prieur S., Caterina D., Primas G.,
 RA Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,
 RA Cohen D.;
 RT "Dense Alu clustering and a potential new member of the NF kappa B
 RT family within a 90 kilobase HLA class III segment.",
 RL Nat. Genet. 3:137-145(1993).
 RN
 RP SEQUENCE FROM N.A.
 RA Neville M.J., Milner C.M., Campbell R.D.;
 RT "A new member of the immunoglobulin superfamily and a V-ATPase G
 RT subunit are amongst the predicted products of novel genes close to the
 RT TNF locus in the human MHC.",
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.
 RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,
 RA Abasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,
 RA Laskey S., Hood L.;
 RT "Sequence of the human major histocompatibility complex class III
 RT region.",
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.
 RA Shiina S., Tamiya G., Oka A., Inoko H.;
 RA "Homo sapiens 2,429,617bp genomic DNA of 6p21.3 HLA class I region.",
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.
 RA Shiina T., Ota M., Katsuyama Y., Hashimoto N., Inoko H.;
 RT "Genome diversity in HLA: a new strategy for detection of genetic
 RT polymorphisms in expressed genes within the HLA class III and class I
 RT regions.",
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.
 RA Rieder M.J., Carrington D.P., Lee K.L., Livingston R.J., Daniels M.R.,
 RA Montoya M.A., Chung M.-W., Yi Q., Miyamoto K.E., Nguyen C.P.,
 RA Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,
 RA Sherwood J.K., Witrak L.A., Nickerson D.A.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Blood;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A.C., Shevchenko Y., Bouffard G.G.,
 RA Whitling M., Madan A., Young A.C., Green E.D., Dickson M.C.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Myers R.M.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Skalska U., Smalls D.E.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Maier M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.",
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN
 RP SEQUENCE OF 77-233 FROM N.A.
 RA Jang J.S., Kim B.E.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN
 RP SEQUENCE OF 84-214 FROM N.A.
 RA Jang J.S., Kim B.E.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN
 RP PHOSPHORYLATION (MEMBRANE FORM).
 RX MEDLINE=96170872; PubMed=8597870;
 RA Pocsik E., Duda E., Wallach D.;
 RT "Phosphorylation of the 26 kDa TNF precursor in monocytic cells and in
 RT transfected HeLa cells.",
 RL J. Inflamm. 45:152-160(1995).
 RN
 RP PHOSPHORYLATION BY CK1, AND DEPHOSPHORYLATION.
 RX MEDLINE=99221647; PubMed=10205166;
 RA Watts A.D., Hunt N.H., Wanigasekara Y., Bloomfield G., Wallach D.,
 RA Routogalis B.D., Chaudhri G.;
 RT "A casein kinase I motif present in the cytoplasmic domain of members
 RT of the tumor necrosis factor ligand family is implicated in 'reverse
 RT signalling'.";
 RL EMBO J. 18:2119-2126(1999).
 RN
 RP MUTAGENESIS.
 RX MEDLINE=91184128; PubMed=2009860;
 RA Octade X.V., Tavernier J., Prange T., Fiers W.;
 RT "Localization of the active site of human tumor necrosis factor
 RT (hTNF) by mutational analysis.",
 RL EMBO J. 10:827-836(1991).
 RN
 RP MYRISTOYLATION.
 RX MEDLINE=93018820; PubMed=1402651;
 RA Stevenson F.R., Bursten S.L., Locksley R.M., Lovett D.H.;
 RT "Myristyl acylation of the tumor necrosis factor alpha precursor on
 RT specific lysine residues.",
 RL J. Exp. Med. 176:1053-1062(1992).
 RN
 RP CLEAVAGE BY ADAM17.
 RX MEDLINE=97186575; PubMed=9034191;
 RA Chen W.-J., Jin S.-L.C., Milla M.E., Burkhardt W., Carter H.L.,
 RA Kost T.A., Lambert M.H., Leesnitzer M.A., McCauley P., McGeehan G.,
 RA Mitchell J., Moyer M., Fabel G., Rocque W., Overton L.K., Schoenen P.,
 RA Seaton T., Su J.-L., Warner J., Willard D., Becherer J.D.;
 RT "Cloning of a disintegrin metalloproteinase that processes precursor
 RT tumour-necrosis factor-alpha.",
 RL Nature 385:733-736(1997).
 RN
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=89159409; PubMed=2922050;
 RA Jones E.V., Stuart D.I., Walker N.P.;
 RT "Structure of tumour necrosis factor.",
 RL Nature 338:225-228(1989).
 RN
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=91193276; PubMed=1964681;


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RA Jones E.Y., Stuart D.I., Walker N.P.;
RT "The structure of tumour necrosis factor -- implications for
RL biological function.";
RJ J. Cell Sci. Suppl. 13:11-18(1990).
RP [23]
RX X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
RA MEDLINE=90008932; PubMed=2551905;
RA Eck M.J., Sprang S.R.;
RT "The structure of tumor necrosis factor-alpha at 2.6-A resolution.
RT Implications for receptor binding.";
RJ J. Biol. Chem. 264:17595-17605(1989).
RN [24]

Query Match      9.6%; Score 123; DB 1; Length 233;
Best Local Similarity 23.0%; Pred. No. 0.0041;
Matches 43; Conservative 32; Mismatches 70; Indels 42; Gaps 8;

QY 80 GPQR-----VAAHITGRGNTLSSPNSK-----NEKALGRKINSWESSRSGH 123
DB 57 GPQREPRDLISPLAQVRSSRT---PSDKPVAHVAVNQAEGQL--QWLNRANA 111
QY 124 SFLSNLHRLNGELVHKEGFYIYSQYFRPQEEIKENTKNDKQMVYIYKYT-----S 177
DB 112 LLANGVELRNLQVLPSEGLYIYSQVLFKQ-----GCPSTHLLTHTISRIASV 162
QY 178 YPDPIILKMSARNCSWK----DAEYGLYSIYOGGIFELKENDRIFSVTNEHLIDMDH 232
DB 163 YQTKVNLISAKSCQRETEGAEAKPWYEPYILGVGFQLEKGRDLSAEINRPDYIDFAE 222
QY 233 EAS--FFG 238
DB 223 SGQVYFG 229

RESULT 13
TNFA CEREL
ID TNFA CEREL STANDARD; PRT; 229 AA.
AC PS1743;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (Cachectin) (fragment).
GN TNF OR TNFSF2 OR TNFA.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_TaxID=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Lockhart E.A.;
RT "Cloning and sequencing of cervine tumor necrosis factor.";
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- DISEASE: Cachexia accompanies a variety of diseases, including
CC cancer and infection, and is characterized by general ill health
CC and malnutrition.
```

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CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U14683; AAA50759.1; -.
DR HSP; P01375; 4TSV.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Signal-anchor.
FT NON_TER 1
FT CHAIN <1 229 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 74 229 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN <1 30 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 31 51 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL).
FT DOMAIN 52 229 EXTRACELLULAR (POTENTIAL).
FT SITE 72 73 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT DISULFID 141 173 BY SIMILARITY.
SQ SEQUENCE 229 AA; 24987 MW; 16DE5F7AA5A7DB35 CRC64;

Query Match      9.5%; Score 122.5; DB 1; Length 229;
Best Local Similarity 22.8%; Pred. No. 0.0044;
Matches 41; Conservative 35; Mismatches 77; Indels 27; Gaps 7;

QY 80 GPQVAAHITGRGNTLSSPNSKNEKALGR-----KINS-----WESSRSGHSFLS 127
DB 52 GPQREQSPGSLGINSPLVQLRSSQASINKPVAHVAVNQAQQLWLDSCANALMAN 111
QY 128 NULHNGELVHKEGFYIYSQYFRPQEEIKENTKNDKQMVYIYK--YTSYPPILLM 185
DB 112 GVKLEDNQLVPTDGLYIYSQVLFKQ-----SCPSTFLTHTISRIASVYQTKVNL 166
QY 186 KSARNSC-----WSKDAEYGLYSIYOGGIFELKENDRIFSVTNEHLIDMDHEAS--FFG 238
DB 167 SAIKSPCHRETPENA-EAKPWYEPYIYOGGVFQLEKGRDLSAEINLPDYLDYAESGVYFG 225

RESULT 14
TNFB HUMAN
ID TNFB HUMAN STANDARD; PRT; 205 AA.
AC P01374; Q9UKS8;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Lymphotoxin-alpha precursor (LT-alpha) (TNF-beta) (Tumor necrosis
DE factor ligand superfamily member 1).
GN LTA OR TNFSF1 OR TNFB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87217060; PubMed=3555974;
RA Nedospasov S.A., Shakhov A.N., Turetskaya R.L., Mett V.A.,
RA Aizov M.M., Georgiev G.P., Korobko V.G., Dobrynin V.N.,
RA Filippov S.A., Syrov N.S., Boldyreva E.F., Chuvpilo S.A.,
RA Chumakov A.M., Shingarova L.N., Ovchinnikov Y.A.;
RT "Tandem arrangement of genes coding for tumor necrosis factor (TNF-
```

alpha) and lymphotoxin (TNF-beta) in the human genome.";
RT Cold Spring Harb. Symp. Quant. Biol. 51:611-624(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86086150; PubMed=3001109;
RA Nedwin G.E., Jarrett-Nedwin J., Smith D.H., Naylor S.L.,
RT Sakaguchi A.Y., Goeddel D.V., Gray P.W.;
RA "Structure and chromosomal localization of the human lymphotoxin
RT gene.";
RN J. Cell. Biochem. 29:171-181(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=87057135; PubMed=3536896;
RA Kobayashi Y., Miyamoto D., Asada M., Obinata M., Osewa T.;
RT "Cloning and expression of human lymphotoxin mRNA derived from a
RT human T cell hybridoma.";
RN J. Biochem. 100:727-733(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=85086243; PubMed=6334807;
RA Gray P.W., Aggarwal B.B., Benton C.V., Bringman T.S., Henzel W.J.,
RT Jarrett J.A., Leung D.W., Moffat B., Ng P., Svedersky L.P.,
RA Palladino M.A., Nedwin G.E.;
RT "Cloning and expression of cDNA for human lymphotoxin, a lymphokine
RT with tumour necrosis activity.";
RN Nature 312:721-724(1984).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=92339500; PubMed=1353024;
RA Matsuyama N., Okawa N., Tsukil Y., Endo T., Kaji A.;
RT "Nucleotide sequence of a cDNA encoding human tumor necrosis factor
RT beta from B lymphoblastoid cell RPMI 1788.";
RN FEBS Lett. 302:141-144(1992).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=93270209; PubMed=8499947;
RA Iris F.J.M., Bougueleret L., Frieur S., Caterina D., Primas G.,
RT Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-W., Dausset J.,
RA Cohen D.;
RT "dense Alu clustering and a potential new member of the NF kappa B
RT family within a 90 kilobase HLA class III segment.";
RN Nat. Genet. 3:137-145(1993).
RN [7]
RP SEQUENCE FROM N.A.
RA Neville M.J., Milner C.M., Campbell R.D.;
RT "A new member of the immunoglobulin superfamily and a V-ATPase G
RT subunit are amongst the predicted products of novel genes close to the
RT TNF locus in the human MHC.";
RN Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RA Shina S., Tamiya G., Oka A., Inoko H.;
RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
RN Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,
RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,
RA Lasky S., Hood L.;
RT "Sequence of the human major histocompatibility complex class III
RT region.";
RN Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A., AND VARIANTS ARG-13; PRO-51 AND ASN-60.
RA Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L.,
RA Poel C.L., Toth E.J., Yi Q., Nickerson D.A.;
RT Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RN [11]
RP PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND VARIANT ASN-60.
RX MEDLINE=93083656; PubMed=1451807;
RA Voigt C.G., Maurer-Fogy I., Adgoff G.R.;
RT "Natural human tumor necrosis factor beta (lymphotoxin). Variable O-
RT glycosylation at Thr7, proteolytic processing, and allelic

variation.";
RT FEBS Lett. 314:85-88(1992).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=92129275; PubMed=1733919;
RA Eck M.J., Ullrich M., Rinderknecht E., de Vos A.M., Sprang S.R.;
RT "The structure of human lymphotoxin (tumor necrosis factor-beta) at
RT 1.9-A resolution.";
RN J. Biol. Chem. 267:2119-2122(1992).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.85 ANGSTROMS) OF 61-205 OF COMPLEX WITH
RN TNFR1.
RX MEDLINE=93258809; PubMed=8387891;
RA Banner D.W., D'Arcy A., Jones W., Gentz R., Schoenfeld H.-J.,
RA Broger C., Lotscher H., Lesslauer W.;
RT "Crystal structure of the soluble human 55 kd TNF receptor-human TNF
RT beta complex: implications for TNF receptor activation.";
RN Cell 73:431-445(1993).
RN [14]
RP VARIANT ASN-60.
RX MEDLINE=91086846; PubMed=1670638;
RA Messer G., Spengler U., Jung M.C., Honold G., Bloemer K., Pape G.R.,
RA Rietmuller G., Weiss E.H.;
RT "Polymorphic structure of the tumor necrosis factor (TNF) locus: an
RT NcoI polymorphism in the first intron of the human TNF-beta gene
RT correlates with a variant amino acid in position 26 and a reduced
RT level of TNF-beta production.";
RN J. Exp. Med. 173:209-219(1991).
RN [15]
RP VARIANT PRO-125.
RX MEDLINE=91139175; PubMed=1671667;
RA Abraham L.J., Du D.C., Zahedi K., Dawkins R.L., Whitehead A.S.;
RT "Haplotypic polymorphisms of the TNFB gene.";
RN Immunogenetics 33:50-53(1991).
CC -1- FUNCTION: Cytokine that in its homotrimeric form binds to
CC TNFRSF1A/TNFR1, TNFRSF1B/TNFR and TNFRSF14/HVEM. In its
CC heterotrimeric form with LTB binds to TNFRSF3/UTER. Lymphotoxin is
CC produced by lymphocytes and cytotoxic for a wide range of tumor
CC cells in vitro and in vivo.
CC -1- SUBUNIT: Homotrimer, and heterotrimer of either two LTB and one
CC LTA subunits or (less prevalent) two LTA and one LTB subunits.
CC -1- SUBCELLULAR LOCATION: Secreted (homotrimer) and membrane-
CC associated (heterotrimers).
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01393; CAA25649.1; -
DR EMBL; X02911; CAA26670.1; -
DR EMBL; D00102; BAA00064.1; -
DR EMBL; M16441; AAG61199.1; -
DR EMBL; D12614; BAA02139.1; -
DR EMBL; M55913; AAB59455.1; -
DR EMBL; Z15026; CAA78746.1; -
DR EMBL; Y14768; CAA75071.1; -
DR EMBL; AP000505; BAB63397.1; -
DR EMBL; AF129756; AAL18092.1; -
DR EMBL; AY070490; AAL49956.1; -
DR EMBL; AY216498; AAO21135.1; -
DR EMBL; A06316; CAA00536.1; -
DR PIR; A92755; QMHUX.
DR PDB; 1TNR; 31-JUL-94.
DR GlycoSuiteDB; P01374; -
DR Genew; HGNC:6709; LTA.
DR MIM; 153440; -
DR GO; GO:0005102; F:receptor binding; TAS.
DR GO; GO:0007267; P:cell-cell signaling; TAS.


```
QY 82 QVAAHITGTRGNT-----LSSPNSKNEKALGRKINSWESSRSHSFSLNHLRNGEL 136
D5 47 QPRAHLTSSASDNRQSDMHQFQDLHOSCHRPVHTW-ANKSFGAHLNMTLTNGRL 105
QY 137 VHEKGFYIYSQYFRF-QBEIKENTKNDQMYYIYKTSYDPDPILLMKSAARNSCWSK 195
D5 106 RVPQDGRYLYSQVYFRYPSPSDSDQSSVSHQVQCYKTKSYLNPIQLKGVGTCKWAP 165
QY 196 DAEGYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASPFAG 240
D5 166 DAAYALHSVYQGGIFELRAGDEVFVSVPSTMVYGEDSSSYFAG 210

RESULT 2
Q9WV90 PRELIMINARY; PRT; 169 AA.
AC Q9WV90 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fas ligand (Fragment).
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20010026; PubMed=10540161;
RA Hodgson P.D., Grant M.D., Michalak T.I.;
RT "Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and
RT chronic woodchuck viral hepatitis.";
RL Clin. Exp. Immunol. 118:63-70(1999).
DR EMBL; AF152368; AAD38387.1; -.
DR HSP; P50591; 1d4V.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0045020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006913; P:apoptosis; IEA.
DR GO; GO:0006955; P:pimmune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS50049; TNF 2; 1.
FT NON_TER 1
FT NON_TER 169
SQ SEQUENCE 169 AA; 19274 MW; FDE3955B014717B6B CRC64;

Query Match 13.6%; Score 175.5; DB 11; Length 169;
Best Local Similarity 27.8%; Pred. No. 5.9e-07;
Matches 54; Conservative 39; Mismatches 58; Indels 43; Gaps 10;

QY 45 QRLQVLRKMLRTSETISTVQKQONISPLVRERGQVAAHITGTRGRNTLSSPNSK 104
D5 10 ELRESIQ---RNTPESL---EKQIGHPSPSPDKALRAAHLT---GKPNRSRSP--- 56
QY 105 NEKALGRKINSWESSRSHSFSLNHLRNGELVHEKGFYIYSQYFRFQBEIKENTKN 164
D5 57 -----LEWEDT-YGSLSGVKYQKGLVINDTGLFYYSKIYFRGQ-----SCN 100
QY 165 DKQMYYIY-KYTSYDPDPILLMK-SARNSC-----WSKDAEYGLYSIYQGGIFELKENDR 217
D5 101 NQPLSHKVYKNSKYPQDLVLMEGKMNYCTTGQWMAR-----SSYLGAVENTFTSNDH 153
QY 218 IFVSVTNEHLIDMD 231
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DB 154 LYVNVSELSLNF 167
Q8MJ19 PRELIMINARY; PRT; 154 AA.
AC Q8MJ19 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Fas ligand CD178 (Fragment).
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA Petit F., Arnould D., Lelievre J.-D., Lecossier D., Hance A.J.,
RA Monceaux V., Ho Tsong Fang R., Hurtrel B., Ameisen J.-C.,
RA Bataquier J.;
RT "Caspase-dependent and -independent cell death pathways characterize
RT pathogenic Simian Immunodeficiency Virus infection. Relationship with
RT disease evolution.";
RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF530076; AAM95636.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:pimmune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR008064; Fas ligand.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01681; FASLIGAND.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF 1; 1.
DR PROSITE; PS50049; TNF 2; 1.
FT NON_TER 1
FT NON_TER 154
SQ SEQUENCE 154 AA; 17410 MW; 971A43779B029449 CRC64;

Query Match 12.2%; Score 157; DB 6; Length 154;
Best Local Similarity 27.4%; Pred. No. 1.9e-05;
Matches 46; Conservative 33; Mismatches 65; Indels 24; Gaps 6;

QY 57 TSEETISTVQKQONISPLVRERGQVAAHITGTRGRNTLSSPNSKNEKALGRKINSW 116
D5 8 TSQKHTASSLEKQIGHPSPPPEKQKVAHLTG-----KPNRSRSP-----EW 52
QY 117 ESSRSGHSFLSNHLRNGELVHEKGFYIYSQYFRFQBEIKENTKNQKQVYIY-KY 175
D5 53 EDT-YGIVLLSGVKYKGLVINETGLFYYSKYFRGQ-----SCTNPLSHKVMRN 105
QY 176 TSYDPDPILLMKSAARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVT 223
D5 106 SKYPQDLVMEGKMNS-ICTTGQWMAHSHSYLGAVENTFTSADHLYVNS 152

RESULT 4
Q7T2Q3 PRELIMINARY; PRT; 227 AA.
AC Q7T2Q3 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Tumor necrosis factor-3 alpha.
OX TNF-3ALPHA.
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OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head kidney;
 RA Saven R., Sakai M.,
 RT "Cloning of tumor necrosis factor 3 alpha in carp."
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB112424; BAC77690.1; -
 SQ SEQUENCE 227 AA; 25226 MW; 010BC2B1E8D7265E CRC64;
 Query Match 11.8%; Score 151.5; DB 13; Length 227;
 Best Local Similarity 25.3%; Pred. No. 8.7e-05;
 Matches 45; Conservative 34; Mismatches 68; Indels 31; Gaps 7;
 QY 75 LVTRERQPVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNG 134
 DB 67 LSKENYTSKVAIHLSGA-----YFDSVSKNNIDWKQNDGAFVSGGLKLVDR 113
 QY 135 ELVIHEKGFYIYSQVFRFQEEIKENTKNDKQVQIYKTSYDPD-----PILLMKSA 188
 DB 114 EIIIPNDGIYIYSQVSFHI--SKNDMTEDQEVHVSNAVHYSDFFGIYK--LIRAA 169
 QY 189 RNSCW----SKDAEYGLIYSQGIIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF 240
 DB 170 RSACVHASNTEDWYD--TIYLGAFSLRAGDKLCTKTITELLPRVETDNKTFEGVF 225
 RESULT 5
 ID 070332 PRELIMINARY; PRT; 216 AA.
 AC 070332;
 DT 01-AUG-1998 (TEMBLrel. 07, Created)
 DT 01-AUG-1998 (TEMBLrel. 07, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Tumor necrosis factor-alpha (Fragment).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Mesocricetus.
 OX NCBI_TaxID=10036;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
 RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
 RT analysis of cytokine mRNA expression in experimental visceral
 RL leishmaniasis."
 RL Infect. Immun. 66:2135-2142(1998).
 DR EMBL; AF046215; AAC40100.1; -
 DR HSP; P06804; 2TNF.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR006053; TNF-abc.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF like.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01234; TNECROSISFCT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS00049; TNF_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 216 AA; 23793 MW; BADAE3F83F45B533 CRC64;

Query Match

11.2%; Score 144.5; DB 11; Length 216;

Best Local Similarity 26.9%; Pred. No. 0.00032;
 Matches 47; Conservative 28; Mismatches 63; Indels 37; Gaps 7;
 QY 80 GQPVAAH---ITGRGRSNTLSSPNSKNEKALGRKINS-----WESSRSGHSFLS 127
 DB 49 GQREKFPNPIGSMGOTLRLSSSSQNSNDKPVGHVVANHQVEQLEWLSHRANALLAN 108
 QY 128 NLHLRNGELVIEHKGFIYSQVFRFQEEIKENTKNDKQVQIYK-----YTSYDP 180
 DB 109 GMSLKDNDQVLPADGLYLVYISQVIFRQ-----GCPSYVLLTHTVSRFAVSVD 157
 QY 181 PILLMKSAENSCWSKDABYV-----LYSIYQGGIFELKENDRIFVSVTNEHLID 229
 DB 158 NVNLLSAIKSPC-PKETPEGEELKWPBYILYGVFQLEKGDRLSAEVLNPKYLD 211

RESULT 6

Q8AW02
 ID Q8AW02 PRELIMINARY; PRT; 231 AA.
 AC Q8AW02;
 DT 01-MAR-2003 (TEMBLrel. 23, Created)
 DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Putative tumour necrosis factor alpha two.
 TNF-ALPHA2PRO.
 OS Cyprinus carpio (Common carp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Cyprinus.
 OX NCBI_TaxID=7962;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Head kidney;
 RA Saelij J.P., Stet R.J., de Vries B., van Muiswinkel W.B.,
 RA Wiegertjes G.F.;
 RT "Molecular and functional characterization of carp TNF: Association of
 RT TNF polymorphism with trypanotolerance."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ311801; CAC84642.2; -
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
 DR GO; GO:0006955; P:immune response; IEA.
 DR InterPro; IPR006053; TNF abc.
 DR InterPro; IPR006052; TNF family.
 DR InterPro; IPR008983; TNF like.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01234; TNECROSISFCT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00049; TNF_2; 1.
 DR PROSITE; PS00049; TNF_2; 1.
 SQ SEQUENCE 231 AA; 25927 MW; 2AD8871D0B1A82F1 CRC64;

Query Match 11.0%; Score 141; DB 13; Length 231;
 Best Local Similarity 23.3%; Pred. No. 0.00068;
 Matches 51; Conservative 38; Mismatches 90; Indels 40; Gaps 9;
 QY 44 WQRLQVRKMLRTSEETISTVQEKQN-----ISPLVREGRQPVAAHITGR 92
 DB 29 WRVCGVLLAVALCAAAAVCFILNKSQNNQEGGNALRLTRDHLKSNVTSKVAIHLTGA- 87
 QY 93 GRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHKGFIYSQVTF 152
 DB 88 -----YDPDVCKDNL-----DMKQNDQAFVSGGLELDVREIIPNDGIYFVSQVSF 135
 QY 153 RQBEIKENTKNDKQV-----QYIKYTSYDDPILLMKSAENSC-WSKDAEYGLY-S 203
 DB 136 HI--SKNDMTEDQVHMSHAVLYSESYGSKYF---LFSAIRSACVHASDSDELWYNT 190
 QY 204 IYQGGIFELKENDRIFVSVTNEHL--IDMDHEASFFGAF 240
 DB 191 IYLGAFNLARDLRTETKELLPRVSENGKTFEGVF 229

PRINTS: PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SMO0207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
FT NON_TER 1 215
SQ SEQUENCE 215 AA; 23696 MW; 3E337E7E65F074EA CRC64;

Query Match 10.5%; Score 135; DB 6; Length 215;
Best Local Similarity 25.3%; Pred. No. 0.002;
Matches 43; Conservative 31; Mismatches 72; Indels 24; Gaps 5;

QY 80 GPQR--VAAHITGTRGRANTLSSPNSKNEKALGRKINS-----WESSRSGHSFSLNL 129
DB 48 GPQRDEFFDNIQLNALLAQTLLRSSTQSDKPAHVAVASIKSEGQLLWSEVANALLANGM 107

QY 130 HLRNGELVTHEKGFYIYSQYVFRQBEIKEN--TKNDKQMVQYIYKYSYPPILLMK 186
DB 108 KLTNDQLVPLDGLYLYISQVLFKQGQCPSTHVFTHNIKRYA-----VSYQKDVLLS 161

QY 187 SARNCSWK-----DAEVLGYSIYOGGIFELKENDRIFVSVTNHELDMD 231
DB 162 AIKSPQSETPEGAGRPWYEPYILGVGFQLEKGRDLSAEINLPDYLD 211

RESULT 10
QY 80 Q9ERG6 PRELIMINARY; PRT; 217 AA.
AC Q9ERG6;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Tumor necrosis factor alpha (Fragment).
OS Peronyscus maniculatus (Deer mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
CX NCBI_TaxID=10042;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Herbst M.M., Schountz T.;
RT "Cloning of the deer mouse interferon gamma, interleukin-10 and tumor
necrosis factor genes."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF307013; AAG30264.1; -
DR HSSP; P06804; 2TNF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF family.
DR InterPro; IPR008983; TNF like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF_1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SMO0207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
FT NON_TER 1 217
SQ SEQUENCE 217 AA; 23964 MW; D6F90C74C0B3021F CRC64;

Query Match 10.5%; Score 135; DB 11; Length 217;
Best Local Similarity 24.7%; Pred. No. 0.002;
Matches 43; Conservative 35; Mismatches 72; Indels 24; Gaps 7;

QY 72 ISPLVRGQRVAAHITGTRGRNTLSSPNSKNEKALGRKINS-----WESSRSG 122
DB 48 IGQREKFPNNLP--IIGSMAQTLTLRSSQSSDKPAHVAVANQVDEQLEWLSRRAN 105

123 HSFSLNHLRNGELVTHEKGFYIYSQYVFRQBEIKENTKNDKQMVQYIYK-TSYDP 181
DB 106 ALLANGMDLKNQVLPADGLYLYISQVLFKQG-----GCSNYLLTHTVSRFAVSDEK 160

QY 182 ILMKSARNCSWKDAEYV-----LYSIYOGGIFELKENDRIFVSVTNHELD 229
DB 161 VNLLSAIKSPC-PKETPEGSELKPWYEPYILGVGFQLEKGRDLSAEVNLPKYLD 213

RESULT 11
QY 80 Q7TIU4 PRELIMINARY; PRT; 222 AA.
AC Q7TIU4;
DT 01-OCT-2003 (TREMELrel. 25, Created)
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Tumor necrosis factor a.
OS Pagrus major (Red sea bream) (Chrysophrys major).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Sparidae; Pagrus.
CX NCBI_TaxID=143350;
RN [1]
RP SEQUENCE FROM N.A.
RA Cai Z., Song L., Gao C., Qiu L., Xiang J.;
RT "Cloning and expression of TNFA from Red Seabream (Pagrus major).";
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY314010; AAP76392.1; -
SQ SEQUENCE 222 AA; 24382 MW; 8D8496F855A552 CRC64;

Query Match 10.1%; Score 130.5; DB 13; Length 222;
Best Local Similarity 24.4%; Pred. No. 0.0049;
Matches 48; Conservative 33; Mismatches 91; Indels 25; Gaps 8;

QY 56 RTSEETISITVQEKQNIPLVRGQRVAAHITGTRGRNTLSSPNSKNEKALGRKINS 115
DB 37 QTALTKIDTAETKIDPHSTLRLRISAKAAHLEGSYDEDE-----GSKDQV-----G 84

QY 116 WESSRSGHSFL-SNLHLRNGELVTHEKGFYIYSQYVFRQ-----BEIKENTKNDKQMVQ 170
DB 85 WKSGQ-QQAFAGGQFRLVDNKVIPQTGLYFYVSQAFVSCSDGEEAGGHTPLSHR 143

QY 171 YIYKYSYPPILLMKSARNCS--WSKDAEY-----GLY-SIYOGGIFELKENDRIFSVT 223
DB 144 ISRSSEMGSDVSLMSAVRSACNTAQDSDSYSGRGWYNTIYLGAVFQLNRGLWTETN 203

QY 224 NEHLIDMDHEASFFGAF 240
DB 204 QLSELETEEGKTFPGVF 220

RESULT 12
QY 80 Q8JG37 PRELIMINARY; PRT; 230 AA.
AC Q8JG37;
DT 01-OCT-2003 (TREMELrel. 22, Created)
DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Tumor necrosis factor.
GN TNF.
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
CX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RA Zou J., Chinchar G., Long S., Miller N., Seconbes C.J.;
RT "Cloning and expression of a tumor necrosis factor homologue in
catfish, Ictalurus punctatus."
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ417565; CAD10389.2; -

```

DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00049; TNF_2; 1.
SQ SEQUENCE 230 AA; 25598 MW; 3A40D391F75DB019 CRC64;

Query Match 9.8%; Score 128; DB 13; Length 230;
Best Local Similarity 29.1%; Pred. No. 0.0082;
Matches 37; Conservative 25; Mismatches 53; Indels 12; Gaps 5;

QY 124 SFSLNHLRNGELVIHEKGFYIYSQTYFRQBEIKENTKNDKQWQVYIKYTSYPPIL 183
DB 104 SFSGKLKEDNEIKLRDLGVYSQASYRLCK-AGDETEGEVHMSHKVSRWSDSYS 162
QY 184 ----LMKSARNSCKDAEYGLY----SIYQGGIFELKENDRIFVSVTNEHLIDMHEA-- 234
DB 163 SWKPLLSATRSACKKTTEBYQWYGVYLGAFNLKAGDRL-RTVMDEKLLPKVESAGG 221
QY 235 -SFFGAF 240
DB 222 KTFPTTF 228

RESULT 13
Q9IB42 PRELIMINARY; PRT; 225 AA.
ID Q9IB42 AC Q9IB42;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Tumor necrosis factor.
OS Paralichthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralichthyidae; Paralichthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20491932; PubMed=11035080;
RA Hirono I., Nam B., Kurobe T., Aoki T.;
RT "Molecular Cloning, Characterization, and Expression of TNF cDNA and
RL Gene from Japanese Flounder Paralichthys olivaceus.";
J. Immunol. 165:4423-4427(2000).
DR HSSP; P01375; 4TSV.
DR EMBL; AB040448; BAA94969.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_subf.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00049; TNF_2; 1.
SQ SEQUENCE 225 AA; 24965 MW; 8F947FB25FC82658 CRC64;

Query Match 9.8%; Score 126.5; DB 13; Length 225;
Best Local Similarity 22.0%; Pred. No. 0.011;
Matches 42; Conservative 40; Mismatches 78; Indels 31; Gaps 8;

QY 67 EKQNTSPLVREGRGPORVAHITGTRGNTLSSPNS---KNEKALGRKINSWESSRSGH 123

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DB 47 ETEPHNTLRQISSAKAAIHLEG-RDEDEBETSENKLVWKNDEGLA-----FTQGGF 98
QY 124 SFSLNHLRNGELVIHEKGFYIYSQTYFRQ-----EIKENTKNDKQWQVY-IKYT 176
DB 99 ELVDN-----HIIPRGLYFVYSQASFRVSCSSDDADGKAAEKHLTGISHRVWLFT 152
QY 177 -SYPPILLMKASRNSCKNS-----KDAEYGLYSTYQGGIFELKENDRIFVSVTNEHLID 229
DB 153 ESLGTQVSLMSAVRSACKSQEDAYRQCGQWYNAILYLGAVFQLNKGDKLWETNMLSELE 212
QY 230 MDHEASFFGAF 240
DB 213 TESGKTFGQVF 223

RESULT 14
Q99ND1 PRELIMINARY; PRT; 215 AA.
ID Q99ND1 AC Q99ND1;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Tumor necrosis factor (Fragment).
OS Tamiasciurus hudsonicus (American red squirrel).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC Tamiasciurus.
OX NCBI_TaxID=10009;
RN [1]
RP SEQUENCE FROM N.A.
RA van Dijk M.A.M., de Jong W.W.;
RT "Indels indicate that rodents are monophyletic and lagomorphs are
RL their sister group.";
Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ286824; CAC28540.1; -.
DR HSSP; P06804; 2TNF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005164; P:tumor necrosis factor receptor binding; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR InterPro; IPR006053; TNF abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR008983; TNF_like.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
FT NON_TER 215
FT NON_TER 215
SQ SEQUENCE 215 AA; 23739 MW; 36441309CA5E9898 CRC64;

Query Match 9.7%; Score 125; DB 11; Length 215;
Best Local Similarity 24.3%; Pred. No. 0.013;
Matches 35; Conservative 29; Mismatches 62; Indels 18; Gaps 4;

QY 99 SPSNKNKALGRKINS-----WESSRSGHFLNHLRNGELVIHEKGFYIYSQTY 151
DB 71 SSSQNMNDKFAHVAVNQTBEQQLNLSRRANALLANGMELIDQLVVPADGLYISQVL 130
QY 152 FRQBEIKENTKNDKQWQVYIKY-TSYPPILLMKASRNSCKNSCKDAEYGLYS-----IY 205
DB 131 FKQ-----CCSSVLLTHTVSRFAVSQYQDKVLLSAIKSPCKESLEGAEFKPWYEPY 185
QY 206 QGGIFELKENDRIFVSVTNEHLID 229
DB 186 LGGVFELQKGRILSAEVLNLPYILD 209

RESULT 15

```

Search completed: June 3, 2004, 09:04:24
Job time : 46 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2004, 08:56:26 ; Search time 59 Seconds
(without alignments)
1163.713 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281
Perfect score: 1287
Sequence: 1 TNELKQMDKYKSGIACFL.....NEHLIDMDHEASFFGAFVVG 243

Scoring table: BLCSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1166853

Minimum DB seq length: 0
Maximum DB seq length: 243

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	953.5	74.1	220	3	AAy88630 Cell fact
2	907	70.5	173	5	Abg72258 Partial h
3	887	68.9	168	4	Abb76826 Human TRA
4	887	68.9	168	5	Aau99896 Human TNF
5	882	68.5	168	5	Abg72259 Partial h
6	878	68.2	166	3	AAb08274 Amino aci
7	866	67.3	167	6	ABR84402 TRAIL ami
8	850	66.0	161	4	AAy71985 C-termina
9	850	66.0	161	6	ABR39855 TNF famil
10	850	66.0	161	7	ADC03335 Tumour ne
11	827	64.3	212	5	AAU99301 Human TRA
12	746.5	58.0	188	5	AAU79599 Human TRA
13	727	56.5	139	2	AAy01518 Polypepti
14	633	49.2	172	3	AAb08275 Amino aci
15	425	33.0	121	3	AAg03752 Human sec
16	370	28.7	113	5	AAU79600 Human TRA
17	291	22.6	98	5	AAU79595 Human TRA
18	291	22.6	101	2	AAW19790 Human apo
19	291	22.6	101	2	AAW56761 Human TRA
20	291	22.6	101	4	AAE11032 Human TRA
21	291	22.6	101	6	ABU08559 Human TNF
22	278	21.6	56	5	AAE23263 Protein #
23	277	21.5	88	5	AAU79594 Human TRA
24	236	18.3	178	6	ADA50080 Human wil
25	233.5	18.1	199	5	ABG94285 Mouse RAN

26 233.5 18.1 199 5 ABG80597
27 232.5 18.1 152 4 AAB67248
28 232.5 18.1 160 3 AAB08273
29 232.5 18.1 185 5 ABG94338
30 232.5 18.1 185 5 ABG80650
31 232.5 18.1 186 5 ABG71829
32 232.5 18.1 200 5 ABG71827
33 232.5 18.1 216 7 ADB16998
34 230.5 17.9 170 4 AAU08386
35 230.5 17.9 216 7 ADB16999
36 228.5 17.8 155 6 ABR39854
37 228.5 17.8 155 7 ADC03334
38 228.5 17.8 160 3 AAB08272
39 228.5 17.8 173 3 AAY84422
40 228.5 17.8 173 3 AAY84421
41 228.5 17.8 187 3 AAY84420
42 219 17.0 139 3 AAY91023
43 210 16.3 182 3 AAY84424
44 208 16.2 188 3 AAY84423
45 202.5 15.7 173 3 AAY84426

ALIGNMENTS

RESULT 1
AAy88630
ID AAY88630 standard; protein; 220 AA.

XX AC AAY88630;

DT 22-AUG-2000 (first entry)

DE Cell factor derivative TRAILD amino acid sequence.

XX Cell factor derivative; TRAILD; anticancer; cancer; liver; breast;

KW kidney; leukaemia.

XX Unidentified.

XX CN1243748-A.

XX 09-FEB-2000.

XX 28-JUL-1999; 99CN-00111039.

XX 28-JUL-1999; 99CN-00111039.

XX (BASI-) INST BASIC MEDICAL SCI CHINESE ACAD MEDI.

XX Zheng D, Liu Y, Ma Z;

XX WFI; 2000-35i201/31.

XX New cell factor derivative causing cells to die, for anticancer therapy.
XX Disclosure; Page 2; 10pp; Chinese.

XX The present invention relates to a cell factor derivative (TRAILD) used as an anticancer derivative. The TRAIL protein can be expressed in a soluble form in bacterial cytoplasm. The present sequence represents a TRAIL amino acid sequence. Recombinant TRAILD fusion proteins can be used in anti-cancer treatments to treat cancer of the liver, breast, or kidney. It can also be used to treat leukaemia

XX Sequence 220 AA;

Query Match 74.1%; Score 953.5; DB 3; Length 220;

Best Local Similarity 97.9%; Pred. No. 7.4e-85;

Matches 185; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 56 RTSETISTYOEKQONISPLVRGPGORVAHITGRGRNTLSSPNKNEKALGRKINS 115
:|||||

Db 32 KTSEETISTVQKQNISPLVRERGQPVAAHITGRSNTLSSPNSKNEKALGRKINS 91
QY 116 WESSRSGHSLNHLRNGELVIH-EKGPVYIYQTYFRQOEIKENTKNDKQWQVIYK 174
Db 92 WESSRSGHSLNHLRNGELVIH-EKGPVYIYQTYFRQOEIKENTKNDKQWQVIYK 151
QY 175 YTSYDPDPILLMKARSNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA 234
Db 152 YTSYDPDPILLMKARSNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEA 211
QY 235 SFFGAFVLG 243
Db 212 SFFGAFVLG 220
RESULT 2
ABG72258
ID ABG72258 standard; protein; 173 AA.
XX AC ABG72258;
XX DT 04-MAR-2003 (first entry)
XX DE Partial human Trail protein, Trail109.
XX KW Human; tumour related apoptosis inducing ligand; Trail109;
XX KW Trail prokaryotic expression system; tumour cell death.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Misc-difference 109
XX FT /note= "Encoded by CTT"
XX FN CN1354183-A.
XX PD 19-JUN-2002.
XX PF 30-NOV-2001; 2001CN-00132371.
XX PR 30-NOV-2001; 2001CN-00132371.
XX PA (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.
XX PI Hu Y, Yao Y;
XX DR WPI: 2002-751439/82.
XX DR N-PSDB; ABX14392.
XX PT Tumor death induction ligand gene, gene expression protein and its
XX PS preparation method.
XX PS Claim 7; Page 10 (disclosure); 17pp; Chinese.
XX CC The present invention relates to the isolation of cDNA encoding human
XX CC tumour related apoptosis inducing ligand (Trail), and the Trail protein.
XX CC The Trail full length cDNA is cloned, and is utilised to create a Trail
XX CC prokaryotic expression system. The full length Trail cDNA is used to
XX CC respectively clone cDNA of soluble ectocytic segment Trail109 and Trail
XX CC 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic
XX CC expression systems. The prokaryotic expression systems created greatly
XX CC increase the expression and quantity of the Trail, Trail109, and Trail114
XX CC proteins, and may be useful in a new preparation for killing tumour
XX CC cells. The present sequence represents the partial human Trail protein,
XX CC Trail109
XX SQ Sequence 173 AA;
Query Match 70.5%; Score 907; DB 5; Length 173;
Best Local Similarity 99.4%; Pred. No. 1.9e-80;
Matches 172; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 71 NISPLVRERGQPVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHL 130

Db 1 NISPLVRERGQPVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHL 60
QY 131 LINGELVTHEKGPVYIYQTYFRQOEIKENTKNDKQWQVIYKTSYDPDPILLMKARSN 190
Db 61 LRNGELVTHEKGPVYIYQTYFRQOEIKENTKNDKQWQVIYKTSYDPDPILLMKARSN 120
QY 191 SCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
Db 121 SCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 173
RESULT 3
ABB76826
ID ABB76826 standard; protein; 168 AA.
XX AC ABB76826;
XX DT 16-JUL-2002 (first entry)
XX DE Human TRAIL.
XX KW Human; TRAIL; tumour necrosis factor; TNF;
XX KW tumour necrosis factor related apoptosis inducing ligand; TRAIL; cancer;
XX KW viral infection; cytostatic.
XX OS Homo sapiens.
XX FN KR2001019100-A.
XX PD 15-MAR-2001.
XX PF 25-AUG-1999; 99XR-00035354.
XX PR 25-AUG-1999; 99XR-00035354.
XX PA (DONG-) DONG WHA PHARM IND CO LTD.
XX PI Cha SS, Kim JU, Lee GJ, Lim GM, Oh BH, Yoon JI, Yoon SJ;
XX DR WPI: 2001-533833/59.
XX DR N-PSDB; ABL53386.
XX PT Producing and crystallizing tumor necrosis factor related apoptosis
XX PS inducing ligand protein, and its three-dimensional structure.
XX PS Claim 1; Page 14; 20pp; Korean.
XX CC The present invention relates to a method for producing Tumour Necrosis
XX CC Factor (TNF) Related Apoptosis Inducing Ligand (TRAIL) protein, and for
XX CC crystallising the TRAIL protein and its three-dimensional structure,
XX CC where the TRAIL protein has improved activity, which specifically kills
XX CC cancer cells and cells infected by virus. The present sequence is human
XX CC TRAIL, which was used in the invention
XX SQ Sequence 168 AA;
Query Match 68.9%; Score 887; DB 4; Length 168;
Best Local Similarity 100.0%; Pred. No. 1.6e-78;
Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 76 VREGQPVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGE 135
Db 1 VREGQPVAAHITGRSNTLSSPNSKNEKALGRKINSWESSRSGHSLNHLRNGE 60
QY 136 LVTHEKGFYIYQTYFRQOEIKENTKNDKQWQVIYKTSYDPDPILLMKARSNSCWSK 195
Db 61 LVTHEKGFYIYQTYFRQOEIKENTKNDKQWQVIYKTSYDPDPILLMKARSNSCWSK 120
QY 196 DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
Db 121 DAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 168

Db 121 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 168

RESULT 5

ABG72259

ID ABG72259 standard; protein; 168 AA.

XX AC ABG72259;

XX DT 04-MAR-2003 (first entry)

XX DE Partial human Trail protein, Trail114.

XX KW Human; tumour related apoptosis inducing ligand; Trail114;

XX OS Trail prokaryotic expression system; tumour cell death.

XX OS Homo sapiens.

XX PH Key

XX FT Misc-difference 104

XX FT /note= "Encoded by CTT"

XX PN CN1354183-A.

XX PD 19-JUN-2002.

XX PF 30-NOV-2001; 2001CN-00132371.

XX PR 30-NOV-2001; 2001CN-00132371.

XX PA (TWOM-) NO 2 MILITARY MEDICAL COLLEGE PLA.

XX PI Hu Y, Yao Y;

XX DR WPI; 2002-751439/82.

XX DR N-PSDB; ABX14393.

XX PT Tumor death induction ligand gene, gene expression protein and its preparation method.

XX PS Claim 7; Page 10 (disclosure); 17pp; Chinese.

XX CC The present invention relates to the isolation of cDNA encoding human tumour related apoptosis inducing ligand (Trail), and the Trail protein. The Trail full length cDNA is cloned, and is utilised to create a Trail prokaryotic expression system. The full length Trail cDNA is used to respectively clone cDNA of soluble ectocytic segment Trail109 and Trail 114, and respectively create Trail109 cDNA and Trail114 cDNA prokaryotic expression systems. The prokaryotic expression systems created greatly increase the expression and quantity of the Trail, Trail109, and Trail114 proteins, and may be useful in a new preparation for killing tumour cells. The present sequence represents the partial human Trail protein, Trail114

XX SQ Sequence 168 AA;

Query Match 68.5%; Score 882; DB 5; Length 168;

Best Local Similarity 99.4%; Pred. No. 5.1e-78;

Matches 167; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 76 VREGRQVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGE 135

DB 1 VREGRQVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGE 60

QY 136 LVIEHKGFFYYISQTYFRFOEIKENTKNDKQVQIYKYTSYDPPILLMKASRNSCWSK 195

DB 61 LVIEHKGFFYYISQTYFRFOEIKENTKNDKQVQIYKYTSYDPPILLMKASRNSCWSK 120

QY 196 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243

DB 121 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 168

RESULT 4

AAU99896

ID AAU99896 standard; protein; 168 AA.

XX AC AAU99896;

XX DT 21-OCT-2002 (first entry)

XX DE Human TNF related apoptosis including ligand (TRAIL) protein.

XX KW TRAIL; TNF receptor apoptosis including ligand; human; SDR5;

XX OS tumour necrosis factor; crystal structure; TRAIL-SDR5 complex; apoptosis.

XX OS Homo sapiens.

XX PN WO200253727-A1.

XX PD 11-JUN-2002.

XX PF 10-JAN-2001; 2001WO-KR000034.

XX PR 29-DEC-2000; 2000KR-00085947.

XX PA (DONG-) DONG WHA PHARM IND CO LTD.

XX PA (UYPO-) UNIV POHANG SCI & TECHNOLOGY.

XX PI Chung YH, Ryu JM, Hwang YH, Yoon JI, Lim KM, Oh B, Cha S;

XX DR WPI; 2002-583613/62.

XX PT Novel expression vector containing an SDR5 encoding gene transformed into Escherichia coli to produce SDR5 protein for crystallizing a tumor necrosis factor-related apoptosis-inducing ligand-SDR5 complex.

XX PS Claim 5; Page 70; 74pp; English.

XX CC This invention relates to an expression vector containing the tumour necrosis factor related apoptosis inducing ligand (TRAIL) protein receptor SDR5. The invention also comprises a method for producing the SDR5 protein from an E. coli transformed with the vector. The method of the invention is useful for crystallizing the TRAIL-SDR5 complex. A TRAIL-SDR5 crystal complex is useful for developing recombinant proteins i.e. proteins with improved stability or cytotoxic activity of a TRAIL protein which involves changing the amino acid of the AA loop to increase the various interactions between amino acids or from the binding site of metal ions or the disulfide bonding, or changing the corresponding amino acids of the homotrimer interface or homodimer interface to increase the various interactions between amino acids or from the binding site of metal ion or disulfide bond, or to fill the cavity. A 3 dimensional structure of the TRAIL-SDR5 complex is useful for the molecular strategy conferring specificity for the recognition between TNF family members and TNF receptor family members and for the development of TRAIL protein, which has a better stable, cytotoxic activity or an improved receptor binding affinity. The present sequence represents the human tumour necrosis factor receptor apoptosis including ligand (TRAIL) protein sequence used in the invention

XX SQ Sequence 168 AA;

Query Match 68.9%; Score 887; DB 5; Length 168;

Best Local Similarity 100.0%; Pred. No. 1.6e-78;

Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 VREGRQVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGE 135

DB 1 VREGRQVAAHITGTRGRSNTLSSPNSKNEALGRKINSWESSRSGHSFSLNHLRNGE 60

QY 136 LVIEHKGFFYYISQTYFRFOEIKENTKNDKQVQIYKYTSYDPPILLMKASRNSCWSK 195

DB 61 LVIEHKGFFYYISQTYFRFOEIKENTKNDKQVQIYKYTSYDPPILLMKASRNSCWSK 120

QY 196 DAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243


```
RESULT 6
AAB08274
ID AAB08274 standard; protein; 166 AA.
XX AC
XX AB08274;
XX DT
XX 04-DEC-2000 (first entry)
XX DE
XX Amino acid sequence of a human TNF ligand TRAIL.
XX AGP-3; tumor necrosis factor ligand; TNF ligand; Crohn's disease;
XX type II transmembrane protein; B cell stimulatory factor;
XX inflammatory disorder; immune disorder; rheumatoid arthritis;
XX lupus and graft versus host disease.
XX OS
XX Homo sapiens.
XX WO200047740-A2.
XX PD
XX 17-AUG-2000.
XX PF
XX 11-FEB-2000; 2000WO-US003653.
XX PR
XX 12-FEB-1999; 9SUS-0119906P.
XX PR
XX 18-NOV-1999; 9SUS-0166271P.
XX XX
XX (AMGE-) AMGEN INC.
XX PA
XX Boyle WJ, Hsu H;
XX PI
XX WPI; 2000-558217/51.
XX DR
XX Novel polypeptides comprising tumor necrosis factor ligand family
XX PT proteins, useful for treating inflammatory and immune disorders, e.g.
XX PT rheumatoid arthritis.
XX PT
XX Claim 14; Fig 9; 71pp; English.
XX XX
XX AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
XX specification describes an AGP-3 polypeptide, which is TNF ligand family
XX member. AGP-3 is a type II transmembrane protein, and is a potent B cell
XX stimulatory factor. Expression of AGP-3 correlates to increases in the
XX number of B cells and immunoglobulins produced. AGP-3 proteins,
XX antibodies, and nucleic acids may be used to treat inflammatory and
XX immune disorders, e.g. rheumatoid arthritis, Crohn's disease, lupus and
XX graft versus host disease. The nucleic acids may be used to regulate the
XX expression of an AGP-3 related protein. The AGP-3 proteins, antibodies
XX and nucleic acids are also useful for the detection of AGP-3 agonists,
XX antagonists and characterizing interactions with AGP-3 related proteins
XX SQ
XX Sequence 166 AA;
XX
XX Query Match 68.2%; Score 878; DB 3; Length 166;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-77; Mismatches 0; Indels 0; Gaps 0;
XX Matches 166; Conservative 0;
XX
XX QY 78 ERGPQVAAHITGRGRNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELV 137
XX DB 1 ERGPQVAAHITGRGRNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNGELV 60
XX
XX QY 138 IHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSKDA 197
XX DB 61 IHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSKDA 120
XX
XX QY 198 EYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
XX DB 121 EYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 166
XX
XX RESULT 7
AABR4402
ID ABR4402 standard; protein; 167 AA.
XX AC
XX ABR4402;
XX DT
XX 09-OCT-2003 (first entry)
XX DE
XX TRAIL amino acid sequence.
XX TRAIL; TNF-related apoptosis-inducing ligand; tumour; necrosis.
XX OS
XX Unidentified.
XX CN1380339-A.
XX PN
XX 20-NOV-2002.
XX PD
XX 10-APR-2001; 2001CN-00105946.
XX PR
XX 10-APR-2001; 2001CN-00105946.
XX PA
XX (CHEN-) CHENGDU DIAO PHARM GROUP CO LTD.
XX PI
XX Li B, Gao X, Liu Z;
XX XX
XX WPI; 2003-230973/23.
XX DR
XX N-PSDB; ACC83357.
XX XX
XX Death induced ligand (TRAIL) cDNA and encoded polypeptide, useful for
XX PT inducing the death of tumor cells, is related to mutational human tumor
XX PT necrosis.
XX PT
XX Claim 4; Fig 2; 14pp; Chinese.
XX XX
XX The invention relates to a TNF-related apoptosis-inducing ligand encoding
XX CC (TRAIL) cDNA and its encoded polypeptide. The gene of the invention is
XX CC related to mutational human tumor necrosis. The polypeptide of the
XX CC invention is useful for inducing the death of tumor cells. The current
XX CC sequence represents the TRAIL amino acid sequence
XX XX
XX Query Match 67.3%; Score 866; DB 6; Length 167;
XX Best Local Similarity 98.2%; Pred. No. 1.9e-76; Mismatches 1; Indels 2; Gaps 1;
XX Matches 166; Conservative 1;
XX
XX QY 75 LVREGPQVAAHITGRGRNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNG 134
XX DB 1 LVREERG--RVAAHITGRGRNTLSSPNSKNEKALGRKINSWESSRSGHSPFLSNLHRLNG 58
XX
XX QY 135 ELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSWS 194
XX DB 59 ELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQMVQYIYKYTSYDPDILLMKSARNCSWS 118
XX
XX QY 195 KDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 243
XX DB 119 KDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFVLG 167
XX
XX RESULT 8
AAY71985
ID AAY71985 standard; protein; 161 AA.
XX AC
XX AAY71985;
XX XX
XX 28-MAR-2001 (first entry)
XX DT
XX C-terminal region of human TRAIL protein.
XX DE
XX Human; Tumour Necrosis Factor; TNF; immunosuppressant; TALL-1;
XX KW Tumour necrosis factor and Apol-related Leucocyte expressed Ligand 1;
XX KW therapy; autoimmune disorder; rheumatoid arthritis; multiple sclerosis;
XX KW systemic lupus erythematosus; SLE; insulin dependent diabetes mellitus;
XX KW thrombocytopenia purpura; acute rheumatic fever; Goodpasture's syndrome;
XX KW haemolytic anaemia; Grave's disease; myasthenia gravis; TRAIL protein;
```

KW post-streptococcal glomerulonephritis; polyarteritis nodosa; BCMA;
XX B cell maturation factor; pemphigus vulgaris; B-lymphocyte proliferation.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 2..8
FT /label= Beta_strand
FT Region 32..34
FT /label= Beta_strand
FT Region 42..44
FT /label= Beta_strand
FT Region 47..50
FT /label= Beta_strand
FT Region 53..56
FT /label= Beta_strand
FT Region 61..72
FT /label= Beta_strand
FT Region 86..91
FT /label= Beta_strand
FT Region 99..109
FT /label= Beta_strand
FT Region 118..128
FT /label= Beta_strand
FT Region 133..143
FT /label= Beta_strand
FT Region 153..160
FT /label= Beta_strand
XX WO20068378-A1.
XX
XX PD 16-NOV-2000.
XX
XX PF 05-MAY-2000; 2000WO-US012266.
XX PF 06-MAY-1999; 99US-0132892P.
XX PR 01-MAY-2000; 2000US-0201012P.
XX
XX (NAJE-) NAT JEWISH MEDICAL & RES CENT.
XX
XX Shu HS;
XX WPI; 2001-016094/02.
XX
XX Isolated TALL-1 protein is used to identify compounds that regulate B
FT lymphocyte proliferation, used to treat B lymphocyte associated
FT autoimmune disorders.
XX
XX Example 1; Fig 1b; 112pp; English.
XX
XX The present invention relates to Tumour necrosis factor (TNF) and ApoL-
CC related leucocyte expressed ligand 1 (TALL-1) nucleic acid molecules,
CC proteins (including homologues), and their antibodies. The invention in
CC particular relates to methods for regulating the interaction between TALL
CC -1 and TALL-1 receptors (BCMA referred as B cell maturation factor) to
CC regulate monocyte, macrophage and B lymphocyte mediated immune responses.
CC TALL-1 protein is useful for identifying compounds that regulate B
CC lymphocyte proliferation. It is also useful for treating B lymphocyte
CC associated autoimmune disorders like rheumatoid arthritis, systemic lupus
CC erythematosus (SLE), insulin dependent diabetes mellitus, multiple
CC sclerosis, myasthenia gravis, Grave's disease, autoimmune haemolytic
CC anaemia, autoimmune thrombocytopenia purpura, Goodpasture's syndrome,
CC pemphigus vulgaris, acute rheumatic fever, post-streptococcal
CC glomerulonephritis, or polyarteritis nodosa. The TALL-1 protein and its
CC corresponding nucleic acid sequence are also useful in diagnostic assays.
CC The present sequence is a C-terminal region of human TRAIL protein, which
CC has 20-25% sequence identity with the C-terminal region of human TALL-1
CC protein extracellular domain. TRAIL protein is a TNF family member
XX
XX Sequence 161 AA;
XX
XX Query Match 66.0%; Score 850; DB 4; Length 161;
XX Best Local Similarity 100.0%; Pred. No. 6.5e-75;
XX Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHGK 142
DB 1 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHGK 60
QY 143 FYIYSOTYPRFQEEIKENTKDKOMQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 202
DB 61 FYIYSOTYPRFQEEIKENTKDKOMQYIYKYTSYDPDPILLMKSARNSCWSKDAEYGLY 120
QY 203 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
DB 121 SIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161
RESULT 9
ABR39855
ID ABR39855 standard; protein; 161 AA.
XX
XX AC ABR39855;
XX
XX DT 11-AUG-2003 (first entry)
XX
XX DE TNF family member, TRAIL (1d4v) protein fragment.
XX
XX KW RANK, receptor activator of necrosis factor kB; RANK ligand; RANKL;
XX KW tumour necrosis factor; TNF; TRAIL; cytokine.
XX
XX OS Unidentified.
XX
XX FN WO2003014077-A2.
XX
XX PD 20-FEB-2003.
XX
XX PF 09-AUG-2002; 2002WO-US025287.
XX
XX PR 09-AUG-2001; 2001US-0311163P.
XX PR 22-MAR-2002; 2002US-00105057.
XX
XX PA (BARN-) BARNES-JEWISH HOSPITAL.
XX
XX PI Lam J, Ross FP, Teitelbaum SL, Nelson CA, Fremont DH;
XX WPI; 2003-256526/25.
XX
XX Composition for identifying a compound with Receptor Activator of
FT Necrosis Factor KB, RANK modulating activity and for identifying RANK or
FT osteoprotegerin modulating compound, has a protein complex in crystalline
FT form.
XX
XX Disclosure; Fig 3; 66pp; English.
XX
XX The invention relates to a composition (I) comprising a protein complex
CC in crystalline form, where the complex comprises an amino acid sequence
CC of a Receptor Activator of Necrosis Factor KB (RANK) Ligand (RANKL)
CC ectodomain. (I) is useful for identifying a compound with RANK modulating
CC activity, and for identifying a RANK or OPG modulating compound. (I) is
CC useful to intelligently design mutants that have altered biological
CC properties and for identifying and/or designing compounds that bind RANK
CC as an approach towards developing new therapeutic agents. (I) is also
CC useful to computationally screen small molecule databases for chemical
CC entities or compounds that can bind in whole, or in part, to RANK or
CC RANKL. The present sequence represents a tumour necrosis factor (TNF)
CC family member, TRAIL (1d4v), used in a structural-based alignment study
CC of murine RANKL protein
XX
XX Sequence 161 AA;
XX
XX Query Match 66.0%; Score 850; DB 6; Length 161;
XX Best Local Similarity 100.0%; Pred. No. 6.5e-75;
XX Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 RVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNHLRNGELVIEHGK 142

Db 1 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHKG 60
QY 143 FYIYISQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 202
Db 61 FYIYISQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 120
QY 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161

RESULT 10
ADC03335
ID ADC03335 standard; protein; 161 AA.
XX
AC ADC03335;
XX
DT 18-DEC-2003 (first entry)
XX
DE Tumour necrosis factor family cytokine, TRAIL.
XX
KW RANKL ectodomain crystal complex; RANK; osteoprotegerin; OPg;
KW bone-forming compound; tumour necrosis factor; TNF family; cytokine;
KW TRAIL.
XX
OS Mus sp.
XX
PN US2003050223-A1.
XX
PD 13-MAR-2003.
XX
PE 09-AUG-2002; 2002US-00215446.
XX
PR 09-AUG-2001; 2001US-0311163P.
XX
PA (LAMJ/) LAM J.
PA (ROSS/) ROSS F P.
PA (TEIT/) TEITELBAUM S L.
PA (NELS/) NELSON C A.
PA (FREM/) FREMONT D H.
XX
FI Lam J, Ross FP, Teitelbaum SL, Nelson CA, Fremont DH;
XX WPI; 2003-605763/57.
XX
XX Composition comprising crystalline receptor activator of NF-kappaB (RANK)
XX ligand ectodomain complex whose three-dimensional structural
XX representation is useful for identifying RANK or osteoprotegerin
XX modulating compound.
XX
XX Disclosure; Fig 3; 40pp; English.
XX
XX The invention relates to a composition comprising a protein complex in
XX crystalline form, where the complex comprises an amino acid sequence of a
XX receptor activator of nuclear factor kappaB (NF-kappaB) (RANK) ligand
XX (RANKL) ectodomain. The three-dimensional structural representation of a
XX RANKL ectodomain crystal complex, is useful for identifying a RANK or
XX osteoprotegerin (OPG) modulating compound, and for identifying a compound
XX with RANK modulating activity. The crystals permit the determination of
XX the three-dimensional X-ray diffraction structure of the crystal-line
XX polypeptide to high resolution. The atomic structure coordinates and
XX structural information which comprises atomic structure coordinates are
XX useful for identifying bone-forming compounds by methods which utilise
XX the coordinates for solving the three-dimensional X-ray diffraction
XX and/or solution structures of other proteins, including mutant forms, to
XX high resolution. The structural information may also be used in a variety
XX of molecular modeling and computer-based screening applications to, for
XX example design mutants of the crystallized RANKL, its receptors, or a
XX portion or fragment of RANKL or its receptors. The coordinates of RANKL
XX crystal, or subsets of such structural coordinates of the RANKL crystal,
XX are useful for designing or identifying candidate compounds capable of
XX modulating RANK biological activity, and for identifying compounds which

CC mimic the capability of RANKL to bind RANK molecules, thereby activating
CC the receptor. The present sequence represents the amino acid sequence of
CC the tumour necrosis factor family cytokine, TRAIL.
XX
SQ Sequence 161 AA;
Query Match 66.0%; Score 850; DB 7; Length 161;
Best Local Similarity 100.0%; Pred. No. 6.5e-75;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 83 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHKG 142
Db 1 RVAAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELVHKG 60
QY 143 FYIYISQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 202
Db 61 FYIYISQTYFRFOEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGLY 120
QY 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243
Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161

RESULT 11
AAU99301
ID AAU99301 standard; protein; 212 AA.
XX
AC AAU99301;
XX
DT 24-SEP-2002 (first entry)
XX
DE Human TRAIL splice variant 8, rpl-6-6, protein.
XX
KW Human; cytostatic; neuroprotective; immunosuppressive; splice variant;
KW tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;
KW TRAIL; apoptosis; programmed cell death; differentiation; development;
KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;
KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;
KW therapeutic; neurodegenerative disease; autoimmune disease; aging;
KW chromosome 3q26; rpl-6-6.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..16 "Cytoplasmic domain"
FT Domain 17..38
FT Domain /note= "Transmembrane domain"
FT Domain 39..212
FT Misc-difference 209 /note= "Extracellular domain"
FT FT /note= "Encoded by in-frame stop codon"
XX
PN US2002061525-A1.
XX
XX 23-MAY-2002.
XX
XX 16-MAY-2001; 2001US-00855544.
XX
XX 16-MAY-2000; 2000IL-00136156.
XX
XX (YELI/) YELIN R.
XX (KHOS/) KHOSRAVI R.
XX (SAVI/) SAVITZKY K.
XX
XX Yelin R, Khosravi R, Savitzky K;
XX WPI; 2002-479259/51.
XX
XX New splice variants of tumor necrosis factor-related apoptosis inducing
XX ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat
XX diseases or disorders associated with low expression of the variants.
XX

PS Claim 4; Fig 8; 29pp; English.

XX The invention discloses isolated, naturally occurring, polypeptide splice variants of human tumor necrosis factor (TNF)-related apoptosis inducing ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal cellular differentiation and development of multicellular organisms.

CC Apoptosis is induced by certain cytokines which include TNF and TRAIL (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane protein which induces apoptosis and nuclear factor-B (NF-B) activation in many tissues and cells. Receptors for TRAIL include two death domain containing receptors, DR4 and DR5, as well as two decoy receptors, DcR1 and DcR2, lacking the intracellular signalling death domain. TRAIL, induced by type I interferons, induces apoptosis in tumour cells, whereas normal cells are relatively resistant without showing significant toxic side effects. Thus, TRAIL has the potential to be a very useful antitumour agent. The naturally occurring splice variants may differ in their cellular distribution, expression levels/timing and activity.

CC Determining these factors could provide possible mechanisms for the induction of apoptosis of tumours cells. The splice variant polypeptides and polynucleotides can be used in gene therapy, to raise antibodies, to detect the levels, distribution and ratios of expression of TRAIL, and its splice variants, in a biological sample and to identify compounds which bind the variant TRAIL products and modulate its activity (agonists and antagonists). Pharmaceutical compositions, comprising an expression vector or any of the amino acid sequences, are useful for causing a cytotoxic effect in cancer cells and for treatment of diseases which can be ameliorated, cured or prevented by lowering or raising the level of the amino acid sequences. The antibodies may also have a therapeutic utility in blocking or decreasing the activity of the TRAIL variant products. Diseases that may be treated include cancer, neurodegenerative diseases, autoimmune diseases, diseases involved in the non-normal development of tissues and aging. TRAIL's gene is located on chromosome 3q26. The sequence presented is the human TNF-related apoptosis inducing ligand (TRAIL) splice variant 8, rpl-6-6, protein which has had an C-terminal section of the conserved TNF domain deleted

XX Sequence 212 AA;

Query Match 64.3%; Score 827; DB 5; Length 212;
Best Local Similarity 91.3%; Pred. No. 1.7e-72;
Matches 158; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 TNELQMDQKYSKSGIACFLKEDSDYDPNDESNVSPCWQVKQLVRKMLRTSEE 60

Db 39 TNELQMDQKYSKSGIACFLKEDSDYDPNDESNVSPCWQVKQLVRKMLRTSEE 98

Qy 61 TISTVQEKQNISPLVRERGPORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120

Db 99 TISTVQEKQNISPLVRERGPORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158

Qy 121 SGHSFLSNLHRLNGELVTHKGFYIYSQTVFRQEEIKENTKXDKQWQVIY 173

Db 159 SGHSFLSNLHRLNGELVTHKGFYIYSQTVFRQEEIKENTKXDKQWQVIY 211

RESULT 12

ID AAU79599

XX AAU79599 standard; protein; 188 AA.

XX AAU79599;

XX 24-SEP-2002 (first entry)

XX Human TRAIL splice variant 6, TRA-33-T7, protein.

KW Human; cytostatic; neuroprotective; immunosuppressive; splice variant; tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand; TRAIL; apoptosis; programmed cell death; differentiation; development; cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B; type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer; therapeutic; neurodegenerative disease; autoimmune disease; aging; chromosome 3q26; TRA-33-T7.

XX

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..116 /note= "Cytoplasmic domain"

FT Domain 17..38 /note= "Transmembrane domain"

FT Domain 39..188 /note= "Extracellular domain"

XX US2002061525-A1.

XX 23-MAY-2002.

XX 16-MAY-2001; 2001US-00855544.

XX 16-MAY-2000; 2000IL-00136156.

XX (YELI/) YELIN R.

PA (KHOS/) KHOSRAVI R.

PA (SAVI/) SAVITZKY K.

PI Yelin R, Khosravi R, Savitzky K;

XX WPI; 2002-479259/51.

XX New splice variants of tumor necrosis factor-related apoptosis inducing ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat diseases or disorders associated with low expression of the variants.

XX Claim 4; Fig 9; 29pp; English.

XX The invention discloses isolated, naturally occurring, polypeptide splice variants of human tumor necrosis factor (TNF)-related apoptosis inducing ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal cellular differentiation and development of multicellular organisms.

CC Apoptosis is induced by certain cytokines which include TNF and TRAIL (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane protein which induces apoptosis and nuclear factor-B (NF-B) activation in many tissues and cells. Receptors for TRAIL include two death domain containing receptors, DR4 and DR5, as well as two decoy receptors, DcR1 and DcR2, lacking the intracellular signalling death domain. TRAIL, induced by type I interferons, induces apoptosis in tumour cells, whereas normal cells are relatively resistant without showing significant toxic side effects. Thus, TRAIL has the potential to be a very useful antitumour agent. The naturally occurring splice variants may differ in their cellular distribution, expression levels/timing and activity.

CC Determining these factors could provide possible mechanisms for the induction of apoptosis of tumours cells. The splice variant polypeptides and polynucleotides can be used in gene therapy, to raise antibodies, to detect the levels, distribution and ratios of expression of TRAIL, and its splice variants, in a biological sample and to identify compounds which bind the variant TRAIL products and modulate its activity (agonists and antagonists). Pharmaceutical compositions, comprising an expression vector or any of the amino acid sequences, are useful for causing a cytotoxic effect in cancer cells and for treatment of diseases which can be ameliorated, cured or prevented by lowering or raising the level of the amino acid sequences. The antibodies may also have a therapeutic utility in blocking or decreasing the activity of the TRAIL variant products. Diseases that may be treated include cancer, neurodegenerative diseases, autoimmune diseases, diseases involved in the non-normal development of tissues and aging. TRAIL's gene is located on chromosome 3q26. The sequence presented is the human TNF-related apoptosis inducing ligand (TRAIL) splice variant 8, rpl-6-6, protein which has had an C-terminal section of the conserved TNF domain deleted

XX Sequence 188 AA;

Query Match 58.0%; Score 746.5; DB 5; Length 188;
Best Local Similarity 61.7%; Pred. No. 1.1e-64;
Matches 150; Conservative 0; Mismatches 0; Indels 93; Gaps 1;

Qy 1 TNELQMDQKYSKSGIACFLKEDSDYDPNDESNVSPCWQVKQLVRKMLRTSEE 60

Db 39 TNELQMDKYSKSGIACFLKEDDSYDPNDEESKNSPCQVQWOLQVRLMFLRTSEE 98
QY 61 TISTVQEQKQNISPLVRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSW 120
Db 99 TISTVQ----- 104
QY 121 SGHSFLSNLHNLGELVTHEKGFYIYSQTYFRQEEIKENTKNDKQWQVIYKTSYD 180
Db 105 -----ENTKNDKQWQVIYKTSYD 125
QY 181 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 136 PILLMKSARNCSWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 185
QY 241 LVG 243
Db 186 LVG 188

RESULT 13
AAV01518
ID AAV01518 standard; peptide; 139 AA.
XX AC AAV01518;
XX DT 27-MAY-1999 (first entry)
XX DE Polypeptide of the invention.
XX KW Neurodegenerative disease; autoimmune disease; inflammatory disease;
KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;
KW surface receptor; TRAIL protein.
XX OS Homo sapiens.
XX PN FR2766713-A1.
XX PD 05-FEB-1999.
XX PF 04-AUG-1997; 97FR-00010176.
XX PR 04-AUG-1997; 97FR-00010176.
XX PA (INMR) BIO MERIEUX.
XX PI Rieger F, Belliveau JF, Perron H;
XX WPI; 1999-156177/14.
XX DR Use of polypeptide derived from TRAIL protein for diagnosis of
PT degenerative disease - autoimmunity and inflammation, also useful in
PT prevention or treatment, and similar use of corresponding ligand and
PT nucleic acid.

XX PS Claim 5; Page 14; 21pp; French.
XX CC The specification describes the use a polypeptide corresponding to at
CC least the primary sequence of part AAV01516-17 to produce a diagnostic,
CC prophylactic or therapeutic composition useful in cases of degenerative,
CC autoimmune and inflammatory diseases. The polypeptides can be used in
CC treatment of neurodegenerative diseases, lupus erythematosus, rheumatoid
CC arthritis, and SEP. The polypeptides are apoptotic in central nervous
CC system cells, antigenic and specifically recognise the surface receptor
CC of the TRAIL protein. The polypeptide is a marker of disease and a
CC therapeutic target, e.g. its apoptotic activity can be blocked with an
CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
CC receptors, inhibiting formation of natural complex. The present sequence
XX represents a polypeptide of the invention
SQ Sequence 139 AA;

Query Match 56.5%; Score 727; DB 2; Length 139;

Best Local Similarity 100.0%; Pred. No. 5.9e-63;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 57 TSEETISTVQEQKQNISPLVRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSW 116
Db 1 TSEETISTVQEQKQNISPLVRERGPQVAAHITGTRGSNTLSSPNSKNEKALGRKINSW 60
QY 117 ESRSCHSFLSNLHNLGELVTHEKGFYIYSQTYFRQEEIKENTKNDKQWQVIYKYT 176
Db 61 ESRSCHSFLSNLHNLGELVTHEKGFYIYSQTYFRQEEIKENTKNDKQWQVIYKYT 120
QY 177 SYDPDPILLMKSARNCSWSK 195
Db 121 SYDPDPILLMKSARNCSWSK 139

RESULT 14
AAB08275
ID AAB08275 standard; protein; 172 AA.
XX AC AAB08275;
XX DT 04-DEC-2000 (first entry)
XX DE Amino acid sequence of a mouse TNF ligand TRAIL.
XX KW AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
KW type II transmembrane protein; B cell stimulatory factor;
KW inflammatory disorder; immune disorder; rheumatoid arthritis;
KW lupus and graft versus host disease.
XX OS Mus sp.
XX PN WO2000047740-A2.
XX PD 17-AUG-2000.
XX PF 11-FEB-2000; 2000WO-US003653.
XX PR 12-FEB-1999; 99US-0119906P.
XX PR 18-NOV-1999; 99US-0166271P.
XX PA (AMGE-) AMGEN INC.
XX PI Boyle WJ, Hsu H;
XX WPI; 2000-556217/51.
XX DR Novel polypeptides comprising tumor necrosis factor ligand family
PT proteins, useful for treating inflammatory and immune disorders, e.g.
PT rheumatoid arthritis.
XX PS Claim 14; Fig 9; 71pp; English.

XX CC AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
CC specification describes an AGP-3 polypeptide, which is TNF ligand family
CC member. AGP-3 is a type II transmembrane protein, and is a potent B cell
CC stimulatory factor. Expression of AGP-3 correlates to increases in the
CC number of B cells and immunoglobulin produced. AGP-3 proteins,
CC antibodies, and nucleic acids may be used to treat inflammatory and
CC immune disorders, e.g. rheumatoid arthritis, Crohn's disease, lupus and
CC graft versus host disease. The nucleic acids may be used to regulate the
CC expression of an AGP-3 related protein. The AGP-3 proteins, antibodies
CC and nucleic acids are also useful for the detection of AGP-3 agonists,
CC antagonists and characterizing interactions with AGP-3 related proteins
XX SQ Sequence 172 AA;

Query Match 49.2%; Score 633; DB 3; Length 172;
Best Local Similarity 71.4%; Pred. No. 1.3e-53;
Matches 120; Conservative 20; Mismatches 22; Indels 6; Gaps 1;

QY 81 PQVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHNLGELVTHE 140

Db 4 POKVAHITGTRNSALIPISKDGLQKIESWESSRKGHSFLNHLVPLNGELVIEQ 63
141 KGFYIYISOTYFRFQEE-----IKENTKNDKQVQYIKYTSYDPDILLMKSAENSCWS 194
64 EGLYIYISOTYFRFQEAEDASAKVSKQVTKQLVQYIYKTSYDPDPIVLMKSAENSCWS 123
195 KDAEYGLYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLV 242
124 RDAEYGLYIYQGGIFELKENDRIFVSVTNEHLMDLDQASFFGAFLI 171

RESULT 15

AAG03752
ID AAG03752 standard; protein; 121 AA.

XX AC AAG03752;

XX DT 06-OCT-2000 (first entry)

XX Human secreted protein, SEQ ID NO: 7833.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping.

XX OS Homo sapiens.

XX PN BP1033401-A2.

XX PD 06-SEP-2000.

XX PF 21-FEB-2000; 2000EP-00200610.

XX PR 26-FEB-1999; 99US-0122487P.

XX PA (GEST) GENSET.

XX PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX DR WPI; 2000-500381/45.

XX DR N-PSDB; AAC03758.

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures.

XX Claim 13; SEQ ID NO 7833; 71pp + Sequence Listing; English.

XX The present sequence is a polypeptide encoded by one of a large number of
XX 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were
XX prepared from total human RNAs or polyA+ RNAs derived from 30 different
XX tissues. EST sequences usually correspond mainly to the 3' untranslated
XX region (UTR) of the mRNA because they are often obtained from oligo-dT
XX primed cDNA libraries. Such ESTs are not well suited for isolating cDNA
XX sequences derived from the 5' ends of mRNAs and even in those cases where
XX longer cDNA sequences have been obtained, the full 5' UTR is rarely
XX included. 5' ESTs are derived from mRNAs with intact 5' ends and can
XX therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs
XX are also used in diagnostic, forensic, gene therapy and chromosome
XX mapping procedures. They are used to obtain upstream regulatory sequences
XX and to design expression and secretion vectors

XX SQ Sequence 121 AA;

Query Match 33.0%; Score 425; DB 3; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.8e-33;
Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDEESNNSFCWQVKQLVKRLMILRTSEE 60
Db 39 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDEESNNSFCWQVKQLVKRLMILRTSEE 98
QY 61 TISTVQEKQONISPLVRERG 80

Db 99 TISTVQEKQONISPLVRERG 118

Search completed: June 3, 2004, 09:02:57
Job time : 61 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2004, 09:04:27 ; Search time 47 Seconds
(without alignments)
1454.581 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281
Perfect score: 1287
Sequence: 1 TNELKQMDKYSKSIACFL.....NEHLIDMDHEASFGAFLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1155919 seqs, 281338677 residues

Total number of hits satisfying chosen parameters: 715872

Minimum DB seq length: 0
Maximum DB seq length: 243

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
2: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
3: /cgn2_6/ptodata/1/pubpaa/US05_PUBCOMB.pcp.*
4: /cgn2_6/ptodata/1/pubpaa/US04_PUBCOMB.pcp.*
5: /cgn2_6/ptodata/1/pubpaa/US03_PUBCOMB.pcp.*
6: /cgn2_6/ptodata/1/pubpaa/US02_PUBCOMB.pcp.*
7: /cgn2_6/ptodata/1/pubpaa/US01_PUBCOMB.pcp.*
8: /cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pcp.*
9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pcp.*
10: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
11: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
12: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
13: /cgn2_6/ptodata/1/pubpaa/US05_PUBCOMB.pcp.*
14: /cgn2_6/ptodata/1/pubpaa/US04_PUBCOMB.pcp.*
15: /cgn2_6/ptodata/1/pubpaa/US03_PUBCOMB.pcp.*
16: /cgn2_6/ptodata/1/pubpaa/US02_PUBCOMB.pcp.*
17: /cgn2_6/ptodata/1/pubpaa/US01_PUBCOMB.pcp.*
18: /cgn2_6/ptodata/1/pubpaa/US00_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	887	68.9	168	9	US-09-900-530A-10
2	878	68.2	166	9	US-09-900-530A-10
3	859	66.7	164	13	US-10-116-378-29
4	850	66.0	161	14	US-10-216-074-7
5	849	66.0	161	14	US-10-338-083-11
6	826	64.2	208	9	US-09-855-544A-16
7	746.5	58.0	188	9	US-09-855-544A-14
8	636	49.4	172	9	US-09-779-050A-17
9	446	34.7	85	14	US-10-286-696-12
10	370	28.7	113	9	US-09-855-544A-15
11	291	22.6	98	9	US-09-855-544A-10
12	291	22.6	101	12	US-10-652-244-4
13	278	21.6	56	15	US-10-399-018-20
14	277	21.5	88	9	US-09-855-544A-9
15	245.5	19.1	87	14	US-10-286-696-13

ALIGNMENTS

RESULT 1		US-09-900-530A-10		US-10-338-785A-2	
		; Sequence 10, Application US/09900530A		Sequence 2, Appli	
		; Patent No. US20020128438A1		Sequence 86, Appl	
		; GENERAL INFORMATION:		Sequence 224, App	
		; APPLICANT: Seol, Dae-Wu		Sequence 10, Appl	
		; APPLICANT: Billiar, Timothy R.		Sequence 84, Appl	
		; TITLE OF INVENTION: DNA Cassette for the Production of		Sequence 15, Appl	
		; TITLE OF INVENTION: Secretable Recombinant Trimeric Trail Proteins, Tetracycline		Sequence 103, App	
		; TITLE OF INVENTION: /Doxycycline-Inducible Adeno-Associated Virus Vector, Their		Sequence 83, Appl	
		; TITLE OF INVENTION: Combination and Use in Gene Therapy		Sequence 100, App	
		; FILE REFERENCE: 5006-1-002		Sequence 320, App	
		; CURRENT APPLICATION NUMBER: US/09/900,530A		Sequence 102, App	
		; CURRENT FILING DATE: 2002-03-19		Sequence 76, Appl	
		; PRIOR APPLICATION NUMBER: KR 2000-38441		Sequence 96, Appl	
		; PRIOR FILING DATE: 2000-07-06		Sequence 14, Appl	
		; NUMBER OF SEQ ID NOS: 48		Sequence 99, Appl	
		; SOFTWARE: FastSeq for Windows Version 4.0		Sequence 2, Appli	
		; SEQ ID NO 10		Sequence 17, Appl	
		; LENGTH: 168		Sequence 24, Appl	
		; TYPE: PRT		Sequence 8, Appli	
		; ORGANISM: homo sapiens		Sequence 5, Appli	
		US-09-900-530A-10		Sequence 3, Appli	
		Query Match 68.9%; Score 887; DB 9; Length 168;		Sequence 1, Appli	
		Best Local Similarity 100.0%; Pred. No. 3.1e-77;			
		Matches 168; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	76	VREGPQVAHIITGRSNTLSSPNKKEALGRKINSWESSRSGHSFLSNLHRLNGE	135		
Db	1	VREGPQVAHIITGRSNTLSSPNKKEALGRKINSWESSRSGHSFLSNLHRLNGE	60		
Qy	136	LVIHEKGPYIYSQTYFRPQBEIKENTKNDQKQVQIYKTYSPDPILLMKGARNCSWSK	195		
Db	61	LVIHEKGPYIYSQTYFRPQBEIKENTKNDQKQVQIYKTYSPDPILLMKGARNCSWSK	120		
Qy	196	DAEYGLIYIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAFLVG	243		

Db 121 DAEGYGLSYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 169

RESULT 2

US-09-779-050A-16

; Sequence 16, Application US/09779050A

; Patent No. US20020160416A1

; GENERAL INFORMATION:

; APPLICANT: BOYLE, WILLIAM

; APPLICANT: HSU, HAILING

; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY

; FILE REFERENCE: A-570B

; CURRENT APPLICATION NUMBER: US/09/779,050A

; CURRENT FILING DATE: 2001-02-12

; PRIOR APPLICATION NUMBER: 60/181,800

; PRIOR FILING DATE: 2000-02-11

; NUMBER OF SEQ ID NOS: 52

; SOFTWARE: Patent in version 3.0

; SEQ ID NO 16

; LENGTH: 166

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-779-050A-16

Query Match 68.2%; Score 878; DB 9; Length 166;

Best Local Similarity 100.0%; Pred. No. 2.2e-76;

Matches 166; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 ERGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELV 137

Db 1 ERGPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELV 60

QY 138 IHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 197

Db 61 IHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 120

QY 198 EYGLSYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243

Db 121 EYGLSYIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 166

RESULT 3

US-10-116-378-29

; Sequence 29, Application US/10116378

; Publication No. US20020150993A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi J.

; APPLICANT: Goddard, Audrey

; APPLICANT: Gurney, Austin

; APPLICANT: Marsters, Scot A.

; APPLICANT: Pitti, Robert M.

; APPLICANT: Wood, William

; TITLE OF INVENTION: NOVEL TUMOR NECROSIS FACTOR RECEPTOR HOMOLOG AND

; TITLE OF INVENTION: NUCLEIC

; FILE REFERENCE: P1206R1

; CURRENT APPLICATION NUMBER: US/10/116,378

; CURRENT FILING DATE: 2002-04-04

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/247,225

; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-09

; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,087

; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-09

; NUMBER OF SEQ ID NOS: 31

; SEQ ID NO 29

; LENGTH: 164

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-116-378-29

Query Match 66.7%; Score 859; DB 13; Length 164;

Best Local Similarity 99.4%; Pred. No. 1.5e-74;

Matches 163; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 80 GPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELV 139

Db 1 GPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELV 60

QY 140 EKGFFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 199

Db 61 EKGFFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 120

QY 200 GLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243

Db 121 GLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 164

RESULT 4

US-10-216-074-7

; Sequence 7, Application US/10216074

; Publication No. US20030148445A1

; GENERAL INFORMATION:

; APPLICANT: Shu, Hong-Bing

; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 2879-72

; CURRENT APPLICATION NUMBER: US/10/216,074

; CURRENT FILING DATE: 2003-03-12

; PRIOR APPLICATION NUMBER: US/09/565,423

; PRIOR FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: UNKNOWN

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: 60/132,892

; PRIOR FILING DATE: 1999-05-06

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 7

; LENGTH: 161

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-216-074-7

Query Match 66.0%; Score 850; DB 14; Length 161;

Best Local Similarity 100.0%; Pred. No. 1.1e-73;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELV 142

Db 1 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELV 60

QY 143 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 202

Db 61 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 120

QY 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243

Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161

RESULT 5

US-10-338-083-11

; Sequence 11, Application US/10338083

; Publication No. US20030166559A1

; GENERAL INFORMATION:

; APPLICANT: Desjarlais, John R.

; APPLICANT: Tansey, Malu Lourdes G.

; APPLICANT: Dahiyat, Bassil I.

; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof

; FILE REFERENCE: A-71273-2

; CURRENT APPLICATION NUMBER: US/10/338,083

; CURRENT FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/345,805

; PRIOR FILING DATE: 2002-01-04

; PRIOR APPLICATION NUMBER: US 60/373,453

; PRIOR FILING DATE: 2002-04-17

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: Patent in version 3.2

QY 80 GPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELV 139

Db 1 GPORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELV 60

QY 140 EKGFFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 199

Db 61 EKGFFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 120

QY 200 GLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243

Db 121 GLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 164

RESULT 4

US-10-216-074-7

; Sequence 7, Application US/10216074

; Publication No. US20030148445A1

; GENERAL INFORMATION:

; APPLICANT: Shu, Hong-Bing

; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 2879-72

; CURRENT APPLICATION NUMBER: US/10/216,074

; CURRENT FILING DATE: 2003-03-12

; PRIOR APPLICATION NUMBER: US/09/565,423

; PRIOR FILING DATE: 2000-05-05

; PRIOR APPLICATION NUMBER: UNKNOWN

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: 60/132,892

; PRIOR FILING DATE: 1999-05-06

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 7

; LENGTH: 161

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-216-074-7

Query Match 66.0%; Score 850; DB 14; Length 161;

Best Local Similarity 100.0%; Pred. No. 1.1e-73;

Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 83 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELV 142

Db 1 RVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSRSGHSFSLNHLRNGELV 60

QY 143 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 202

Db 61 FYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDPDPILLMKSARNCSWSDA 120

QY 203 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 243

Db 121 SIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFLVG 161

RESULT 5

US-10-338-083-11

; Sequence 11, Application US/10338083

; Publication No. US20030166559A1

; GENERAL INFORMATION:

; APPLICANT: Desjarlais, John R.

; APPLICANT: Tansey, Malu Lourdes G.

; APPLICANT: Dahiyat, Bassil I.

; TITLE OF INVENTION: Dominant Negative Proteins and Methods Thereof

; FILE REFERENCE: A-71273-2

; CURRENT APPLICATION NUMBER: US/10/338,083

; CURRENT FILING DATE: 2003-01-15

; PRIOR APPLICATION NUMBER: US 60/345,805

; PRIOR FILING DATE: 2002-01-04

; PRIOR APPLICATION NUMBER: US 60/373,453

; PRIOR FILING DATE: 2002-04-17

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: Patent in version 3.2

; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-083-11

Query Match
Best Local Similarity 58.0%; Score 746.5; DB 9; Length 188;
Matches 150; Conservative 0; Mismatches 0; Indels 93; Gaps 1;

Qy 1 TNELKQMDKYSGKGIACFLKEDDSYDNDDESMNSPCWQVQWQLRQLVRKMLRTSEE 60
Db 39 TNELKQMDKYSGKGIACFLKEDDSYDNDDESMNSPCWQVQWQLRQLVRKMLRTSEE 98
Qy 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQ-----104
Qy 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYDP 180
Db 105 -----ENTKNDKQWQYIYKYTSYDP 125
Qy 181 PILLMKSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 126 PILLMKSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 185
Qy 241 LVG 243
Db 186 LVG 188

RESULT 8
US-09-779-050A-17
; Sequence 17, Application US/09779050A
; Patent No. US20020160416A1
; GENERAL INFORMATION:
; APPLICANT: BOYLE, WILLIAM
; APPLICANT: HSU, HAILING
; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
; FILE REFERENCE: A-570B
; CURRENT APPLICATION NUMBER: US/09/779,050A
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: 60/181,800
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 17
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-779-050A-17

Query Match
Best Local Similarity 49.4%; Score 636; DB 9; Length 172;
Matches 120; Conservative 20; Mismatches 22; Indels 6; Gaps 1;

Qy 81 PORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHE 140
Db 4 PORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHE 63
Qy 141 KGFYIYSQTYFRFQBE-----IKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWS 194
Db 64 EGLYIYSQTYFRFQBEADASKMVKDKVTKQLVQYIYKYTSYDPDILLMKSARNSCWS 123
Qy 195 KDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 242
Db 124 RDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 171

RESULT 9
US-10-286-696-12
; Sequence 12, Application US/10286696
; Publication No. US20030129706A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K

; SEQ ID NO 11
; LENGTH: 161
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-083-11

Query Match
Best Local Similarity 66.0%; Score 849; DB 14; Length 161;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 82 ORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEK 141
Db 1 QVAAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVIHEK 60
Qy 142 GFYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGL 201
Db 61 GFYIYSQTYFRFQBEIKENTKNDKQWQYIYKYTSYDPDILLMKSARNSCWSKDAEYGL 120
Qy 202 YSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 242
Db 121 YSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 161

RESULT 6
US-09-855-544A-16
; Sequence 16, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 16
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-16

Query Match
Best Local Similarity 64.2%; Score 826; DB 9; Length 208;
Matches 156; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGKGIACFLKEDDSYDNDDESMNSPCWQVQWQLRQLVRKMLRTSEE 60
Db 39 TNELKQMDKYSGKGIACFLKEDDSYDNDDESMNSPCWQVQWQLRQLVRKMLRTSEE 98
Qy 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
Qy 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENT 162
Db 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQBEIKENT 200

RESULT 7
US-09-855-544A-14
; Sequence 14, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 14
; LENGTH: 188
; TYPE: PRT

```
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. US20030129706A1el Member of the TNF Ligand Supergene F
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/10/286,696
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-286-696-12

Query Match      34.7%; Score 446; DB 14; Length 85;
Best Local Similarity 100.0%; Pred. No. 3.4e-35;
Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 ERGPQVAHITGTRGSRNTLSPNSKNEKALGRKINSWESSRSGHSLNHLRANGELV 137
DB 1 ERGPQVAHITGTRGSRNTLSPNSKNEKALGRKINSWESSRSGHSLNHLRANGELV 60

QY 138 IHEKGFYIYSQTYFRFQBEIKENT 162
DB 61 IHEKGFYIYSQTYFRFQBEIKENT 85

RESULT 10
US-09-855-544A-15
; Sequence 15, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-15

Query Match      28.7%; Score 370; DB 9; Length 113;
Best Local Similarity 100.0%; Pred. No. 1e-27;
Matches 69; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGSGIACFLKEDDSYWDPNDESMNSPCQVQKWLRLVRLVRLTSEE 60
DB 39 TNELKQMDKYSGSGIACFLKEDDSYWDPNDESMNSPCQVQKWLRLVRLVRLTSEE 98

QY 61 TISTVQEKQ 69
DB 99 TISTVQEKQ 107

RESULT 11
US-09-855-544A-10
; Sequence 10, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 98

; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 101
; TYPE: PRT
; ORGANISM: human
US-10-652-244-4

Query Match      22.6%; Score 291; DB 12; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.6e-20;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGSGIACFLKEDDSYWDPNDESMNSPCQVQKWLRLVRLVRLV 52
DB 39 TNELKQMDKYSGSGIACFLKEDDSYWDPNDESMNSPCQVQKWLRLVRLVRLV 90

RESULT 12
US-10-652-244-4
; Sequence 4, Application US/10652244
; Publication No. US20040052788A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/10/652,244
; CURRENT FILING DATE: 2003-09-02
; PRIOR APPLICATION NUMBER: US/09/796,581
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 101
; TYPE: PRT
; ORGANISM: human
US-10-652-244-4

Query Match      22.6%; Score 291; DB 12; Length 101;
Best Local Similarity 100.0%; Pred. No. 3.6e-20;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGSGIACFLKEDDSYWDPNDESMNSPCQVQKWLRLVRLVRLV 52
DB 39 TNELKQMDKYSGSGIACFLKEDDSYWDPNDESMNSPCQVQKWLRLVRLVRLV 90

RESULT 13
US-10-399-018-20
; Sequence 20, Application US/10399018
; Publication No. US20040002118A1
; GENERAL INFORMATION:
; APPLICANT: Smilansky, Zeev
; TITLE OF INVENTION: METHOD FOR DETERMINING MASS ALTERING MOIETY IN PEPTIDES
; FILE REFERENCE: 9124.137USWO
; CURRENT APPLICATION NUMBER: US/10/399,018
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/IL01/00944
; PRIOR FILING DATE: 2001-10-11
; PRIOR APPLICATION NUMBER: IL138946
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 56
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Search completed: June 3, 2004, 09:10:17
Job time : 47 secs

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-399-018-20

Query Match      21.6%; Score 278; DB 15; Length 56;
Best Local Similarity 100.0%; Pred. No. 2.9e-19;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 RTSEETISTVQEKQONTSPILVRERGPOVAHAHITGRGRSNTLSSPNSKNEKALGR 111
Db 1 RTSEETISTVQEKQONTSPILVRERGPOVAHAHITGRGRSNTLSSPNSKNEKALGR 56
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RESULT 14
US-09-855-544A-9
; Sequence 9, Application US/09855544A
; Patent No. US20020061525A1
; GENERAL INFORMATION:
; APPLICANT: Rodrigo YELIN et al.
; TITLE OF INVENTION: SEQUENCES OF TRAIL VARIANTS
; FILE REFERENCE: 2786-0173P
; CURRENT APPLICATION NUMBER: US/09/855,544A
; CURRENT FILING DATE: 2001-05-19
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-855-544A-9
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Query Match      21.5%; Score 277; DB 9; Length 88;
Best Local Similarity 100.0%; Pred. No. 6.7e-19;
Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQWDKYSKSGIACFLKEDDSYWDPNDEESMNSPCQVQWKQLRQL 49
Db 39 TNELKQWDKYSKSGIACFLKEDDSYWDPNDEESMNSPCQVQWKQLRQL 87
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RESULT 15
US-10-286-656-13
; Sequence 13, Application US/10286696
; Publication No. US20030129706A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fm, A No. US20030129706A1e1 Member of the TNF Ligand Supergene
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/10/286,696
; CURRENT FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mouse
US-10-286-696-13
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Query Match      19.1%; Score 245.5; DB 14; Length 87;
Best Local Similarity 65.8%; Pred. No. 7.1e-16;
Matches 50; Conservative 9; Mismatches 14; Indels 3; Gaps 1;

Qy 81 PQVAHAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVIEH 140
Db 4 PQVAHAHITGRGRSNTLSSPNSKNEKALGRKINSWESSRSGHFLSNLHRLNGELVIEQ 63

Qy 141 KGFYIYSQTYRFOE 156
Db 64 E---YIYSQTYRFOE 76
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OK protein - protein search, using sw model

Run on: June 3, 2004, 09:01:51 ; Search time 22 Seconds
(without alignments)
570.232 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281

Perfect score: 1287
Sequence: 1 TNELKQMDKYSKGIACFL.....NEHLIDMDHEASFFQAFVLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 317993

Minimum DB seq length: 0

Maximum DB seq length: 243

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/2/iaa/5B COMB.pap.*
- 3: /cgn2_6/ptodata/2/iaa/6A COMB.pap.*
- 4: /cgn2_6/ptodata/2/iaa/6B COMB.pap.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	930	72.3	177	3	US-09-105-343A-7
2	850	66.0	161	4	US-09-585-423-7
3	654	50.8	183	3	US-09-105-343A-8
4	446	34.7	85	4	US-09-632-287A-12
5	291	22.6	101	1	US-08-670-354-4
6	291	22.6	101	3	US-09-320-424-4
7	291	22.6	101	4	US-09-825-563-4
8	291	22.6	101	5	PCT-US96-10895-4
9	245.5	19.1	87	4	US-09-632-287A-13
10	228.5	17.8	173	4	US-09-396-937-10
11	228.5	17.8	173	4	US-09-396-937-12
12	228.5	17.8	187	4	US-09-396-937-8
13	210	16.3	182	4	US-09-396-937-16
14	208	16.2	188	4	US-09-396-937-14
15	202.5	15.7	173	4	US-09-396-937-20
16	195.5	15.2	173	4	US-09-396-937-18
17	189.5	14.7	179	4	US-08-339-214-22
18	182	14.1	138	4	US-08-339-214-20
19	181.5	14.1	178	4	US-08-339-214-84
20	181.5	14.1	179	3	US-08-649-100-9
21	181.5	14.1	179	4	US-08-339-214-6
22	179	13.9	137	4	US-08-339-214-18
23	178	13.8	145	3	US-08-630-172-5
24	178	13.8	145	3	US-09-375-419-5
25	177.5	13.8	179	4	US-08-339-214-14
26	175.5	13.6	149	3	US-08-584-031-17
27	175	13.6	152	4	US-09-496-118B-8

Sequence 4, Appli
Sequence 12, Appli
Sequence 81, Appli
Sequence 5, Appli
Sequence 80, Appli
Sequence 4, Appli
Sequence 22, Appli
Sequence 79, Appli
Sequence 83, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 10, Appli
Sequence 82, Appli
Sequence 1, Appli
Sequence 4, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 39, Appli

28 173 13.4 138 4 US-08-339-214-4
29 173 13.4 138 4 US-08-339-214-12
30 173 13.4 138 4 US-08-339-214-81
31 173 13.4 138 4 US-09-565-423-5
32 173 13.4 139 4 US-08-339-214-80
33 173 13.4 139 4 US-08-968-686-4
34 173 13.4 141 3 US-09-286-529-22
35 173 13.4 141 4 US-08-339-214-79
36 170 13.2 136 4 US-08-339-214-83
37 170 13.2 136 4 US-08-968-686-8
38 170 13.2 137 4 US-08-339-214-2
39 170 13.2 137 4 US-08-339-214-10
40 170 13.2 137 4 US-08-339-214-82
41 161.5 12.5 240 3 US-08-943-014A-1
42 161.5 12.5 240 4 US-09-072-993C-4
43 161.5 12.5 240 4 US-09-653-285-1
44 160 12.4 174 4 US-09-131-237C-2
45 159.5 12.4 208 4 US-09-027-287-39

ALIGNMENTS

RESULT 1
US-09-105-343A-7
; Sequence 7, Application US/09105343A
; Patent No. 6207642
; GENERAL INFORMATION:
; APPLICANT: WILEY, S.R.
; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
; FOR TREATMENT AND DIAGNOSIS OF DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-6050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09105343A
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/02859
; FILING DATE: 12-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, Cheryl L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 6048.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-938-1729
; TELEFAX: 847-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 177 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6207642e
US-09-105-343A-7

Query Match 72.3%; Score 930; DB 3; Length 177;
Best Local Similarity 99.4%; Pred. No. 1.2e-88;
Matches 176; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 67 EKOQNSPLVREGPORVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSRSHSFL 126

Db 1 EKQONISPLVRERGQORVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFL 60
 Qy 127 SNLHRLNGELVTHKGFYIYSQTYFRQBEIKENTKDKOMVOYIYKYTSYDPILLMK 186
 Db 61 SNLHRLNGELVTHKGFYIYSQTYFRQBEIKENTKDKOMVOYIYKYTSYDPILLMK 120
 Qy 187 SARNCSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAPLVG 243
 Db 121 SARNCSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAPLVG 177

RESULT 2

US-09-565-423-7
 ; Sequence 7, Application US/09565423
 ; Patent No. 6475987
 ; GENERAL INFORMATION:
 ; APPLICANT: Shu, Hong-Bing
 ; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
 ; FILE OF INVENTION: METHODS OF USE THEREOF
 ; FILE REFERENCE: 2879-72
 ; CURRENT APPLICATION NUMBER: US/09/565,423
 ; CURRENT FILING DATE: 2000-05-05
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/132,892
 ; PRIOR FILING DATE: 1999-05-06
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 161
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-565-423-7

Query Match 66.0%; Score 850; DB 4; Length 161;
 Best Local Similarity 100.0%; Pred. No. 2.1e-80;
 Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 83 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHK 142
 Db 1 RVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELVTHK 60
 Qy 143 FYIYSQTYFRQBEIKENTKDKOMVOYIYKYTSYDPILLMKSAARNCSKDAEYGLY 202
 Db 61 FYIYSQTYFRQBEIKENTKDKOMVOYIYKYTSYDPILLMKSAARNCSKDAEYGLY 120
 Qy 203 SIYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAPLVG 243
 Db 121 SIYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAPLVG 161

RESULT 3

US-09-105-343A-8
 ; Sequence 8, Application US/09105343A
 ; Patent No. 6207642
 ; GENERAL INFORMATION:
 ; APPLICANT: WILEY, S.R.
 ; TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
 ; FILE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Abbott Laboratories
 ; STREET: 100 Abbott Park Road
 ; CITY: Abbott Park
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60064-6050
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows
 ; SOFTWARE: Fast-SEQ for Windows Version 2.0b

; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/105,343A
 ; FILING DATE: 12-FEB-1998
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US98/02859
 ; FILING DATE: 12-FEB-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BECKER, Cheryl L.
 ; REGISTRATION NUMBER: 35,441
 ; REFERENCE/DOCKET NUMBER: 6048.US.P2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 847-935-1729
 ; TELEFAX: 847-938-2623
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 183 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: No. 6207642e
 ; US-09-105-343A-8
 Query Match 50.8%; Score 654; DB 3; Length 183;
 Best Local Similarity 68.7%; Pred. No. 5.6e-60;
 Matches 125; Conservative 22; Mismatches 29; Indels 6; Gaps 1;
 Qy 67 EKQONISPLVRERGQORVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFL 126
 Db 1 EKQSTPPLPRGGRPKVAAHITGTRRSNSALIPISKDGKTLGOKIESWESSRSGHSFL 60
 Qy 127 SNLHRLNGELVTHKGFYIYSQTYFRQBEIKENTKDKOMVOYIYKYTSYDP 180
 Db 61 NHVLFNGELVTHKGFYIYSQTYFRQBEIKENTKDKOMVOYIYKYTSYDP 120
 Qy 181 PILLMKSAARNCSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAP 240
 Db 121 PIVLAKSARNCSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLMDHDEASFFGAP 180
 Qy 241 LV 242
 Db 181 II 182

RESULT 4

US-09-632-287A-12
 ; Sequence 12, Application US/09632287A
 ; Patent No. 6521422
 ; GENERAL INFORMATION:
 ; APPLICANT: Hsu, Hailing
 ; APPLICANT: Wooden, Scott X
 ; APPLICANT: Boyle, William J
 ; TITLE OF INVENTION: Fhm, A No. 6521422a1 Member of the TNF Ligand Supergene Family
 ; FILE REFERENCE: 01017/35550A
 ; CURRENT APPLICATION NUMBER: US/09/632,287A
 ; CURRENT FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: US 60/147,294
 ; PRIOR FILING DATE: 1999-08-04
 ; NUMBER OF SEQ ID NOS: 22
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 12
 ; LENGTH: 85
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-632-287A-12
 Query Match 34.7%; Score 446; DB 4; Length 85;
 Best Local Similarity 100.0%; Pred. No. 7.1e-39;
 Matches 85; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 78 ERQPRVAAHITGRGSRNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHRLNGELV 137

Db 1 ERGPORVAHITGTGRSNTLSGPNKNEKALGRKINSWESSRSGHSFLSNLHNRNGELV 60

Qy 138 IHEKGFYIYSQTYFRQBEIKENT 162
Db 61 IHEKGFYIYSQTYFRQBEIKENT 85

RESULT 5

US-08-670-354-4
; Sequence 4, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 101 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-4

Query Match 22.6%; Score 291; DB 1; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRLVRK 52
Db 39 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRLVRK 90

RESULT 6

US-09-320-424-4
; Sequence 4, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis

; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; CURRENT FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 101
; TYPE: PRT
; ORGANISM: human
US-09-320-424-4

Query Match 22.6%; Score 291; DB 3; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRLVRK 52
Db 39 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRLVRK 90

RESULT 7

US-09-825-563-4
; Sequence 4, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 101
; TYPE: PRT
; ORGANISM: human
US-09-825-563-4

Query Match 22.6%; Score 291; DB 4; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRLVRK 52
Db 39 TNELKQMDKYSGKGIACFLKEDDSYWDPNDEESMNSPCWQVKWQLRLVRK 90

RESULT 8

PCT-US96-10895-4
; Sequence 4, Application PC/TUS9610895

GENERAL INFORMATION:
APPLICANT: Immunex Corporation.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.5.2
SOFTWARE: Microsoft Word, Version 6.0.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10895
FILING DATE: 25-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,632
FILING DATE: 29-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/548,368
FILING DATE: 01-NOV-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2835-WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 101 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10895-4

Query Match 22.6%; Score 291; DB 5; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDNDEESVNSPCQVKWQLRQLVRK 52
|||||
Db 39 TNELKQMDKYSKSGIACFLKEDDSYWDNDEESVNSPCQVKWQLRQLVRK 90
|||||

RESULT 9
US-09-632-287A-13
; Sequence 13, Application US/09632287A
; Patent No. 6521422
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; APPLICANT: Wooden, Scott K
; APPLICANT: Boyle, William J
; TITLE OF INVENTION: Fhm, A No. 6521422e1 Member of the TNF Ligand Supergene Family
; FILE REFERENCE: 01017/35550A
; CURRENT APPLICATION NUMBER: US/09/632,287A
; CURRENT FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/147,294
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Mouse

US-09-632-287A-13

Query Match 19.1%; Score 245.5; DB 4; Length 87;
Best Local Similarity 65.8%; Pred. No. 4.7e-18;
Matches 50; Conservative 9; Mismatches 14; Indels 3; Gaps 1;
QY 81 PQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEH 140
|||||
Db 4 PQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEH 140
|||||

QY 141 KGFYIYSQTYFRFQE 156
: |||||
Db 64 E--YIYSQTYFRFQE 76
: |||||

RESULT 10
US-09-396-937-10
; Sequence 10, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA encoding
; OTHER INFORMATION: murine OPG, residues 158-316, fused to His tag
US-09-396-937-10

Query Match 17.8%; Score 228.5; DB 4; Length 173;
Best Local Similarity 34.2%; Pred. No. 7.4e-16;
Matches 54; Conservative 31; Mismatches 62; Indels 11; Gaps 4;

QY 86 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHKGFFY 145
|||||
Db 22 AHITGTRGRSNTLSSPNSKNEKALGRKINSWESSRSGHSFLSNLHLRNGELVIEHKGFFY 145
|||||
QY 146 IYSQTYFRFQEIKENTKNDKQMVQYIYKYT-SYDPILLMKSRNSCWSDAEYGLYSI 204
|||||
Db 72 LYANICFRHETSGSVPTDYLQLMVYVVKTSIKIPSSHNLKMGKSTKNWGNSEPHFYSI 131
|||||
QY 205 YQGGIFELKENDRIFVSVTNEHLIDMDHEASFGATLV 242
|||||
Db 132 NVGGFFKLAGEEISIQVSNPSLLDPDQDATYFGAFKV 169
|||||

RESULT 11
US-09-396-937-12
; Sequence 12, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 173

QY 189 RNSCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 242
Db 131 HLENWGSNSEHFYSINVGGFFKLAGEEISIQVSNPSLLDPDQDATYFGAFV 184

RESULT 15

US-09-396-937-20
; Sequence 20, Application US/09396937
; Patent No. 6645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC.1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion between
; OTHER INFORMATION: murine OPG, residues 158-316 with tetanus toxoid
; OTHER INFORMATION: P30 epitope introduced, and His tag
US-09-396-937-20

Query Match 15.7%; Score 202.5; DB 4; Length 173;
Best Local Similarity 30.2%; Pred. No. 3.7e-13;
Matches 52; Conservative 28; Mismatches 53; Indels 39; Gaps 5;
QY 86 AHITGRGRSNTLSPPNSKNEKALGRKINSWESSRSGHSFLGNLHRLNGELVIHEKGFY 145
Db 22 AHLT-----INAAISFGSHKVTL---SSWYHDR-GWAKISMTLSNGKLAVNQDGFY 71
QY 146 IYSQTYR-----FQEIKNKDKQMVQYIKYTSYPPDILLMKARN 190
Db 72 LYANICFNFTVSFWLRVPKVSASHLEVKTSIK-----IPSSENLMKGGST 117
QY 191 SCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAFV 242
Db 118 KWSGNSSEHFYSINVGGFFKLAGEEISIQVSNPSLLDPDQDATYFGAFV 169

Search completed: June 3, 2004, 09:05:32
Job time : 23 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 3, 2004, 11:26:36 ; Search time 60 Seconds
(without alignments)
1144.317 Million cell updates/sec

Title: US-10-662-430-2_COPY39_281

Perfect score: 1287
Sequence: 1 TNELKQMDKYSGKIACFL.....NEHLIDMDHEASFGAFLVG 243

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseqp29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1287	100.0	279	2 AAW76332	AAW76332 Human TL2
2	1287	100.0	279	2 AAW95032	AAW95032 Tumour ne
3	1287	100.0	281	2 AAW19777	AAW19777 Novel cyt
4	1287	100.0	281	2 AAW27134	AAW27134 Human Apo
5	1287	100.0	281	2 AAW19787	AAW19787 Human Apo
6	1287	100.0	281	2 AAW76829	AAW76829 Human TL2
7	1287	100.0	281	2 AAW56760	AAW56760 Human TRA
8	1287	100.0	281	2 AAW44354	AAW44354 Human AGP
9	1287	100.0	281	2 AAY01517	AAY01517 Protein a
10	1287	100.0	281	2 AAY27012	AAY27012 Human Apo
11	1287	100.0	281	3 AAY81956	AAY81956 Human Apo
12	1287	100.0	281	3 AAB24038	AAB24038 Human PRO
13	1287	100.0	281	3 AAB08545	AAB08545 Amino aci
14	1287	100.0	281	3 AAB28691	AAB28691 Human AGP
15	1287	100.0	281	4 AAB50977	AAB50977 Human PRO
16	1287	100.0	281	4 AAB67243	AAB67243 Human Apo
17	1287	100.0	281	4 AAE11031	AAE11031 Human TNF
18	1287	100.0	281	4 AAB48350	AAB48350 Human TL2
19	1287	100.0	281	5 ABB08133	ABB08133 Human TRA
20	1287	100.0	281	5 ABG31630	ABG31630 Human TRA
21	1287	100.0	281	5 AAU75062	AAU75062 Human TNF
22	1287	100.0	281	5 AAM51077	AAM51077 Human Apo
23	1287	100.0	281	5 ABP51954	ABP51954 Human Apo
24	1287	100.0	281	5 AAO19095	AAO19095 C neofom
25	1287	100.0	281	5 AAU79593	AAU79593 Human TNF

26	1287	100.0	281	6 ABG73861	ABG73861 Human Apo
27	1287	100.0	281	6 ABU10205	ABU10205 Human Apo
28	1287	100.0	281	6 ABU71443	ABU71443 Human neo
29	1287	100.0	281	6 ABG72738	ABG72738 Human TNF
30	1287	100.0	281	6 AAO29543	AAO29543 Human TRA
31	1287	100.0	281	6 ABU08558	ABU08558 Human TNF
32	1287	100.0	281	6 ABR42313	ABR42313 Human TRA
33	1287	100.0	281	6 ABG71905	ABG71905 Human TRA
34	1287	100.0	281	6 ABP60546	ABP60546 Human tum
35	1287	100.0	281	6 AAB36258	AAB36258 Human TR4
36	1287	100.0	281	6 AAO31151	AAO31151 Human TNF
37	1287	100.0	281	6 ABO25125	ABO25125 Human TNF
38	1287	100.0	281	7 AD861471	AD861471 Native hu
39	1287	100.0	281	7 ADC35202	ADC35202 Human TNF
40	1287	100.0	281	7 ADD14080	ADD14080 Human SRC
41	1287	100.0	281	7 ADD19010	ADD19010 Human dis
42	1287	100.0	281	8 AD876953	AD876953 Human pro
43	1284	99.6	281	7 AD861488	AD861488 Human Apo
44	1282	99.6	266	4 AAY72935	AAY72935 OmpA sign
45	1282	99.6	281	5 ABG72257	ABG72257 Human tum

ALIGNMENTS

RESULT 1

AAW76332
ID AAW76332 standard; protein; 279 AA.

XX AAW76332;

XX AC

XX DT 11-JAN-1999 (first entry)

XX DE Human TL2 (TRAIL), ligand for TR5.

XX KW TL2; TRAIL; tumour necrosis related receptor; TR5; inflammation;
KW arthritis; septicaemia; transplant rejection; autoimmune disease;
KW inflammatory bowel disease; graft versus host disease; infection; stroke;
KW ischaemia; acute respiratory disease syndrome; psoriasis; restenosis;
KW brain injury; AIDS; bone disease; cancer; atherosclerosis;
KW Alzheimer's disease; human; therapy; diagnosis; ligand.

XX OS Homo sapiens.

XX PN EP867509-A2.

XX PD 30-SEP-1998.

XX PF 04-FEB-1998; 98EP-00300827.

XX PR 05-FEB-1997; 97US-00795910.

XX PR 28-JUL-1997; 97US-00901469.

XX PA (SMK) SMITHKLINE BEECHAM CORP.

XX PI Young PR, Tan KB, Truneh A, Lyn SDP;

XX WPI; 1998-497862/43.

XX New polynucleotide encoding TR5 polypeptide - used to diagnose, prevent
PT and treat e.g. inflammation, arthritis, septicaemia, autoimmune diseases,
PT infections, stroke, ischaemia, ARDS, psoriasis, restenosis, brain injury,
PT AIDS and bone diseases.

XX PS Disclosure; Page 17-18; 22pp; English.

XX This is the amino acid sequence of human TL2 (also known as TRAIL), which
CC has newly been discovered to be a ligand of human tumour necrosis related
CC receptor TR5 (see AAW76331). This TR5 polypeptide of the invention and
CC TL2 can be used in screening processes for compounds which bind the
CC receptor, or its ligand, and which activate (agonists) or inhibit
CC (antagonists) the receptor or TL2. Treatment of a subject with the need
CC to inhibit TR5 polypeptide activity comprises administering an antagonist

CC to the polypeptide, administering a nucleic acid that inhibits the
 CC expression of the nucleotide sequence encoding the polypeptide and/or
 CC administering a polypeptide that competes with the polypeptide for its
 CC ligand, substrate or receptor. The active agents can be used for the
 CC treatment of chronic and acute inflammation, arthritis, septicemia,
 CC autoimmune diseases (e.g. inflammatory bowel disease, psoriasis),
 CC transplant rejection, graft vs host disease, infection, stroke,
 CC ischaemia, acute respiratory disease syndrome, restenosis, brain injury,
 CC AIDS, bone diseases, cancer (e.g. lymphoproliferative disorders),
 CC atherosclerosis and Alzheimer's disease
 XX
 SQ Sequence 279 AA;

Query Match 100.0%; Score 1287; DB 2; Length 279;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESNPCWQVQWQLRQVVKMLRTSEE 60
 DB 37 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESNPCWQVQWQLRQVVKMLRTSEE 96
 QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSR 120
 DB 97 TISTVQEKQONISPLVRERGPQVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSR 156
 QY 121 SGHSFLSNLHRLNGELVIEHKGFPYIYSQTYFRFOEIKENTKNDKQWQVYIKYTSYD 180
 DB 157 SGHSFLSNLHRLNGELVIEHKGFPYIYSQTYFRFOEIKENTKNDKQWQVYIKYTSYD 216
 QY 181 PILLMKSARNCSWCKDAEYGLSYIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 217 PILLMKSARNCSWCKDAEYGLSYIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 276
 QY 241 LVG 243
 DB 277 LVG 279

RESULT 2

AAW95032
 ID AAW95032 standard; protein; 279 AA.

AC AAW95032;

DT 13-MAY-1999 (first entry)

XX Tumour necrosis factor receptor (TNF-R) related polypeptide TL2.

XX Tumour necrosis factor receptor; TNF-R; TR1; TR2; TL2; TL4; arthritis;
 XX inflammation; septicemia; autoimmune disease; transplant rejection;
 XX graft vs. host disease; infection; stroke; ischemia; brain injury; AIDS;
 XX acute respiratory disease syndrome; restenosis; bone disease; cancer;
 XX atherosclerosis; Alzheimer's disease.

XX Unidentified.

XX EP897114-A2.

XX 17-FEB-1999.

XX 04-JUN-1998; 98EP-00304424.

XX 13-AUG-1997; 97US-0055513P.

XX 26-AUG-1997; 97US-0056980P.

XX 29-AUG-1997; 97US-0057550P.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Brigham-Burke MR, Young PR;

XX WPI; 1999-134308/12.

XX Identifying agonists and antagonists to tumour necrosis factor receptor

PT (TNF-R) related polypeptides (LR1, LR2, LR2 and LR4) - useful for
 PT treating stroke, Alzheimer's disease and AIDS.
 XX
 PS Disclosure; Page 14-15; 18pp; English.

CC The invention relates to identifying agonists or antagonists to tumour
 CC necrosis factor receptor (TNF-R) related polypeptides (TR1 and TR2, TL2
 CC and TL4). The method comprises: (a) (i) contacting TR1 or TR2 with a
 CC candidate compound in the presence of TL2 or TL4; or (ii) contacting TL2
 CC or TL4 with a candidate compound in the presence of TR1 or TR2; and (b)
 CC assessing the ability of the candidate compound to compete with TR1 or
 CC TR2 binding to TL2 or TL4. TR and TL agonists and antagonists are useful
 CC for treating diseases caused by imbalance of TL or TR polypeptide levels,
 CC which cause chronic and acute inflammation, arthritis, septicemia,
 CC autoimmune diseases, transplant rejection, graft vs. host disease,
 CC infection, stroke, ischemia, acute respiratory disease syndrome,
 CC restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis and
 CC Alzheimer's disease. The present sequence represents a TNF-R related
 CC polypeptide TL2
 XX
 SQ Sequence 279 AA;

Query Match 100.0%; Score 1287; DB 2; Length 279;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESNPCWQVQWQLRQVVKMLRTSEE 60
 DB 37 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESNPCWQVQWQLRQVVKMLRTSEE 96
 QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSR 120
 DB 97 TISTVQEKQONISPLVRERGPQVAAHITGTRGRNTLSSPNKNEKALGRKINSWESSR 156
 QY 121 SGHSFLSNLHRLNGELVIEHKGFPYIYSQTYFRFOEIKENTKNDKQWQVYIKYTSYD 180
 DB 157 SGHSFLSNLHRLNGELVIEHKGFPYIYSQTYFRFOEIKENTKNDKQWQVYIKYTSYD 216
 QY 181 PILLMKSARNCSWCKDAEYGLSYIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 217 PILLMKSARNCSWCKDAEYGLSYIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 276
 QY 241 LVG 243
 DB 277 LVG 279

RESULT 3

AAW19777

ID AAW19777 standard; protein; 281 AA.

XX AAW19777;

XX 22-SEP-1997 (first entry)

XX Novel cytokine Apo-2 ligand.

XX Apo-2 ligand; cytokine; apoptosis; breast cancer; colon cancer; therapy.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..281 /note= "Claim 4"

FT Region 1..14 /label= Cytoplasmic_region

FT Protein 15..281 /note= "Claim 3"

FT Region 15..40 /label= Transmembrane_region

FT Protein 41..281 /note= "Claim 2"

FT Region 41..281

```

FT Modified-site /label= Extracellular_region
FT 109
FT /label= Glycosylation
FT /note= "putative N-linked glycosylation site"
FT Protein 114. .281
FT /note= "Claim 1"
XX
XX WO9725428-A1.
XX
XX 17-JUL-1997.
XX
XX 08-JAN-1997; 97WO-US000272.
XX
XX 09-JAN-1996; 96US-00584031.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Chuntharapai A, Kim KJ;
XX WPI; 1997-372867/34.
XX N-PSDB; AAT72796.
XX
XX Novel cytokine, Apo-2 ligand and corresponding DNA - used to induce
XX apoptosis for the treatment of breast and colon cancer.
XX
XX Claim 4; Fig 1a; 72pp; English.
XX
XX A novel cytokine (AAW1977), designated Apo-2 ligand, induces mammalian
XX cell apoptosis. It is believed to be a member of the tumour necrosis
XX factor cytokine family. Its amino acid sequence was deduced from a cDNA
XX clone (AA72796) isolated from a human placental cDNA library. Apo-2
XX ligand polypeptides, esp. those corresponding to amino acids 114-281, 41-
XX 281, 15-281 or 1-281 of Apo-2 ligand, can be produced by culturing cells
XX transformed or transfected with a vector contg. Apo-2 ligand nucleic
XX acid. They can be used to induce apoptosis in mammals and to treat
XX pathological conditions such as cancer (esp. breast or colon cancer) or
XX to raise antibodies useful in diagnostic assays
XX
XX Sequence 281 AA;
XX
XX Query Match 100.0%; Score 1287; DB 2; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-117;
XX Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TNELKQMDKYSKSGIACFLKEDDSYNDPNDSESMNSPCWQVKQLRQLVKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYNDPNDSESMNSPCWQVKQLRQLVKMLRTSEE 98
XX
QY 61 TISTVQEKQONISPLVREGRGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVREGRGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
XX
QY 121 SGHSFLSNLHLNGLVHIEKGFYIYSQTYFRFOBEIKENTKNDKQWQVIYKITSYDP 180
DB 159 SGHSFLSNLHLNGLVHIEKGFYIYSQTYFRFOBEIKENTKNDKQWQVIYKITSYDP 218
XX
QY 181 PILLMKSARNSCWSKDAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNSCWSKDAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
XX
QY 241 LVG 243
DB 279 LVG 281
XX
RESULT 4
AAW27134
ID AAW27134 standard; protein; 281 AA.
XX
XX AAW27134;
XX
XX 02-APR-1998 (first entry)
XX

```

```

DE Human Apoptosis inducing molecule-I (AIM-I).
XX
XX Apoptosis inducing molecule-I; AIM-I; autoimmune disorder;
XX tumour necrosis factor ligand superfamily; AIM-I altered expression;
XX neoplasia inhibition; anti-inflammatory agent.
XX
XX Homo sapiens.
XX
XX WO9733899-A1.
XX
XX 18-SEP-1997.
XX
XX 14-MAR-1996; 96WO-US003773.
XX
XX 14-MAR-1996; 96WO-US003773.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM;
XX
XX WPI; 1997-470807/43.
XX N-PSDB; AAT85210.
XX
XX New isolated apoptosis inducing molecule-I - used to develop products for
XX the diagnosis and therapy of e.g. autoimmune diseases, tumours, graft
XX versus host disease or inflammation.
XX
XX Claim 2; Fig 1; 82pp; English.
XX
XX The present sequence represents a human Apoptosis inducing molecule-I
XX (AIM-I). AIM-I is a member of the tumour necrosis factor (TNF) ligand of
XX superfamily. The products can be used in the diagnosis and treatment of
XX disorders related to under-expression, over-expression or altered
XX expression of AIM-I. AIM-I or agonists can be used for treating
XX autoimmune disorders including systemic lupus erythematosus,
XX immunoproliferative disease lymphadenopathy (IPT),
XX angioimmunoproliferative lymphadenopathy (AIL), rheumatoid arthritis,
XX diabetes, and multiple sclerosis, graft versus host disease, to inhibit
XX haematopoiesis in endothelial cell development, to stimulate peripheral
XX tolerance and cytotoxic T-cell mediated apoptosis. Antagonists can be
XX used for treating cachexia, cerebral malaria, rheumatoid arthritis or
XX osteoporosis, for preventing graft-host rejection, and as anti-
XX inflammatory agents, for treating endotoxic shock or to prevent
XX activation of HIV
XX
XX Sequence 281 AA;
XX
XX Query Match 100.0%; Score 1287; DB 2; Length 281;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-117;
XX Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TNELKQMDKYSKSGIACFLKEDDSYNDPNDSESMNSPCWQVKQLRQLVKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYNDPNDSESMNSPCWQVKQLRQLVKMLRTSEE 98
XX
QY 61 TISTVQEKQONISPLVREGRGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVREGRGPORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
XX
QY 121 SGHSFLSNLHLNGLVHIEKGFYIYSQTYFRFOBEIKENTKNDKQWQVIYKITSYDP 180
DB 159 SGHSFLSNLHLNGLVHIEKGFYIYSQTYFRFOBEIKENTKNDKQWQVIYKITSYDP 218
XX
QY 181 PILLMKSARNSCWSKDAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNSCWSKDAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
XX
QY 241 LVG 243
DB 279 LVG 281
XX

```

RESULT 5
AAW19787
ID AAW19787 standard; protein; 281 AA.
XX
AC AAW19787;
XX
DT 24-SEP-1997 (first entry)
XX
DE Human apoptosis inducer cytokine TRAIL.
XX
KW Tumour necrosis factor related apoptosis inducing ligand; TRAIL;
XX cytokine; cancer; leukaemia; lymphoma; melanoma; viral infection;
KW thrombotic microangioplasty; therapy.
XX
OS Homo sapiens.
XX
FH Key
FT Domain
FT /label= Cytoplasmic_domain
FT /label= Transmembrane_domain
FT /label= Extracellular_domain
FT /note= "contains a receptor-binding region"
FT Cleavage-site 39..90
FT /note= "potential KEX2 protease processing site"
FT Modified-site 109..111
FT /note= "potential N-glycosylation site"
FT Cleavage-site 149..150
FT /note= "potential KEX2 protease processing site"
XX WC09701633-AL.
XX
RD 16-JAN-1997.
XX
XX 25-JUN-1996; 96WO-US010895.
XX
PR 29-JUN-1995; 95US-00496632.
PR 01-NOV-1995; 95US-00548368.
XX
PA (IMMV) IMMUNEX CORP.
XX
XX Wiley SR, Goodwin RG;
XX
DR WPI; 1997-118715/11.
DR N-PSDB; AAW72847.
XX
XX TRAIL, a novel cytokine, induces apoptosis in cancer and virus-infected
XX cells - useful for treating thrombotic microangiopathy, cancer and viral
XX infection and for use in assays.
XX
PS Claim 10; Page 43-44; 62pp; English.
XX
CC Human tumour necrosis factor related apoptosis inducing ligand (TRAIL)
CC (AAW19787) is a novel cytokine that induces apoptosis of certain target
CC cells, including cancer cells and virally infected cells. Its amino acid
CC sequence was deduced from cDNA clone HuAIC (AAW72848), deposited in
CC vector pDC409 as ATCC 69849. Recombinant TRAIL polypeptides (esp. soluble
CC polypeptides) can be expressed in host cells and used in the treatment of
CC cancer (e.g. leukaemia, lymphoma and melanoma) and viral infections, or
CC to raise antibodies that may be useful for treating thrombotic
CC microangiopathies
XX
SQ Sequence 281 AA;
XX
Query Match 100.0%; Score 1287; DB 2; Length 281;
Best Local Similarity 100.0%; Pred No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVQLRQLVKKMLRTSEE 60
DB 39 TNELKQMDKYKSGIACFLKEDDSYWDPNDEESMNSPCWQVQLRQLVKKMLRTSEE 98

QY 61 TISTVQEKQONISPLVREGRGPQVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVREGRGPQVAAHITGTRGRSNTLSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVIEHKGFFYYISQTYFFQBEIEKENTKNDQMVQYIYKYTSYPD 180
DB 159 SGHSFSLNHLRNGELVIEHKGFFYYISQTYFFQBEIEKENTKNDQMVQYIYKYTSYPD 218
QY 181 PILLMKSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF 240
DB 219 PILLMKSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF 278
QY 241 LVG 243
DB 279 LVG 281
XX
RESULT 6
AAW76829
ID AAW76829 standard; protein; 281 AA.
XX
AC AAW76829;
XX
DT 25-JAN-1999 (first entry)
XX
DE Human TL2 protein.
XX
KW TR6; tumour necrosis factor related receptor; human; treatment; stroke;
KW inflammation; arthritis; septicemia; autoimmune disease; restenosis;
KW transplant rejection; infection; ischaemia; brain injury; bone disease;
KW acute respiratory disease syndrome; acquired autoimmune disease syndrome;
KW AIDS; cancer; atherosclerosis; Alzheimers disease; TRAIL; TNF;
KW TL2. tumour necrosis factor-related apoptosis-inducing ligand.
XX
OS Homo sapiens.
XX
PN EP870827-A2.
XX
PD 14-OCT-1998.
XX
PF 23-DEC-1997; 97EP-00310562.
XX
XX 14-MAR-1997; 97US-0041230P.
XX 09-MAY-1997; 97US-00853684.
XX 22-AUG-1997; 97US-00916625.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Deen KC, Young PR;
XX
DR WPI; 1998-523156/45.
DR N-PSDB; AAV63095.
XX
XX DNA encoding tumour necrosis factor receptor TR6 - and corresponding
XX polypeptide, antibody, agonist, antagonist, etc.
XX
PS Disclosure; Page 32-33; 34pp; English.
XX
CC This sequence represents the human tumour necrosis factor (TNF)-related
CC receptor TL2 (also known as tumour necrosis factor-related apoptosis-
CC inducing ligand, TRAIL). This protein is used in a method resulting in
CC the isolation of the novel human TNF related receptor, TR6. TR6
CC polypeptides and polynucleotides can be used in the treatment of chronic
CC and acute inflammation, arthritis, septicemia, autoimmune diseases (e.g.
CC inflammatory bowel disease, psoriasis), transplant rejection, graft vs.
CC host disease, infection, stroke, ischaemia, acute respiratory disease
CC syndrome, restenosis, brain injury, (acquired autoimmune disease
CC syndrome) AIDS, bone diseases, cancer (e.g. lympho-proliferative
CC disorders), atherosclerosis and Alzheimers disease
XX
SQ Sequence 281 AA;
XX
Query Match 100.0%; Score 1287; DB 2; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.3e-117; Mismatches 0; Indels 0; Gaps 0; Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESMNSPCWQVQWLRQLVRKMLRTSEE 60
 DB 39 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESMNSPCWQVQWLRQLVRKMLRTSEE 98

QY 61 TISTVQEKQONISPLVREGRPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSR 120
 DB 99 TISTVQEKQONISPLVREGRPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOBEIKENTKNDKQWQVYIYKTSYPD 180
 DB 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOBEIKENTKNDKQWQVYIYKTSYPD 218

QY 181 PILLMKSARNCSWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKSARNCSWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
 DB 279 LVG 281

RESULT 7
 ID AAW56760 standard; protein; 281 AA.
 AC AAW56760;
 DT 05-AUG-1998 (first entry)
 DE Human TRAIL polypeptide.
 KW Tumour necrosis factor related apoptosis ligand; TRAIL; research; human; cytokine; therapy; leukaemia; lymphoma; melanoma; viral infection.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 1..18 /note= "N-terminal cytoplasmic domain"
 FT Region 19..38 /note= "transmembrane region"
 FT Domain 39..281 /note= "extracellular domain"

US5763223-A.
 PN 09-JUN-1998.
 PD 25-JUN-1996; 96US-00670354.
 PF 29-JUN-1995; 95US-00496632.
 PR 01-NOV-1995; 95US-00548368.
 XX (IMMV) IMMUNEX CORP.
 PI Goodwin RG, Wiley SR;
 XX WPI; 1998-347322/30.
 DR N-PSDB; AAV29518.
 XX DNA encoding cytokine TNF-related apoptosis ligand polypeptides - useful for producing recombinant polypeptides for research and therapy of leukaemia, lymphoma, melanoma and viral infections.
 PS Claim 1; Col 33-36; 28pp; English.
 CC This represents a human tumour necrosis factor related apoptosis ligand (TRAIL) polypeptide. The human and murine TRAIL polypeptides can induce apoptosis of Jurkat cells. The encoding nucleic acid sequences are useful for producing the recombinant TRAIL polypeptides, which may be useful in

CC studies of apoptosis, to purify leukaemia, lymphoma or melanoma cells (e.g. to isolate antigens for vaccine development). The polypeptides can be used to treat leukaemia, lymphoma or melanoma (e.g. by extracorporeal treatment of blood or bone-marrow), or to treat viral infections

QY 1 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESMNSPCWQVQWLRQLVRKMLRTSEE 60
 DB 39 TNELKQMDKYSGKGIACFLKEDDSYWDPNDESMNSPCWQVQWLRQLVRKMLRTSEE 98

QY 61 TISTVQEKQONISPLVREGRPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSR 120
 DB 99 TISTVQEKQONISPLVREGRPQVAAHITGTRGSRNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOBEIKENTKNDKQWQVYIYKTSYPD 180
 DB 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOBEIKENTKNDKQWQVYIYKTSYPD 218

QY 181 PILLMKSARNCSWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKSARNCSWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
 DB 279 LVG 281

RESULT 8
 ID AAW44354 standard; protein; 281 AA.
 AC AAW44354;
 DT 28-MAY-1998 (first entry)
 DE Human AGP-1.
 KW Human; AGP-1; tumour necrosis factor-related protein; TNF; inflammation; bone resorption; haematopoietic disease.
 OS Homo sapiens.
 FN WO9746686-A2.
 XX PD 11-DEC-1997.
 XX 06-JUN-1997; 97WO-US009895.
 PF 07-JUN-1996; 96US-00660562.
 XX (AMGE-) AMGEN INC.
 PI Johnson MJ, Simonet WS, Danilenko DM;
 XX WPI; 1998-042194/04.
 DR N-PSDB; AAV15295.
 XX Nucleic acid encoding AGP-1, a tumour necrosis factor-related protein - useful for treating inflammation, bone resorption and haematopoietic diseases.
 PS Claim 7; Page 36-37; 54pp; English.
 CC The present sequence represents human AGP-1. AGP-1 is a tumour-necrosis factor (TNF)-related protein, involved in inflammation, myelopoiesis and bone resorption. It has the same nucleic acid and amino acid (aa) sequences as the TNF-related apoptosis-induced ligand (TRAIL) described in Immunity, 3 (1995) 673. Antibodies (Ab) are used as immunoassay

CC reagents for detecting AGP-1 expression. Nucleic acid complementary to
CC AGP-1 is used to regulate AGP-1 expression and antagonistic compounds are
CC used to treat inflammation (e.g. rheumatoid arthritis, systemic lupus
CC erythematosus, psoriasis, scleroderma, infection-related inflammation) or
CC bone resorption diseases (e.g. osteoporosis, osteomyelitis,
CC hypercalcaemia, Paget's disease). AGP-1 can be used to treat
CC haematopoietic diseases associated with reduction in the number of bone
CC marrow cells, particularly neutrophils and lymphocytes, e.g. where caused
CC by disease, injury or exposure to myelosuppressive agents. Host cells,
CC transformed with expression vectors containing AGP-1 DNA, are used to
CC produce recombinant AGP-1
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMDKYSGKGIACFLKEDDSYWDNDDESNPCQVQKWLRLVVKMLRTSEE 60
DB 39 TNELKQMDKYSGKGIACFLKEDDSYWDNDDESNPCQVQKWLRLVVKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVIEHKGFIYYSQTYFRFOEIKENTKNDKQVQYIYKITSYD 180
DB 159 SGHSFSLNHLRNGELVIEHKGFIYYSQTYFRFOEIKENTKNDKQVQYIYKITSYD 218
QY 181 PILLMKSARNCSWKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 9
AAY01517
ID AAY01517 standard; peptide; 281 AA.
XX
AC AAY01517;
XX
DT 27-MAY-1999 (first entry)
XX
DE Protein associated with neurodegenerative and autoimmune diseases.
XX
KW Neurodegenerative disease; autoimmune disease; inflammatory disease;
KW lupus erythematosus; rheumatoid arthritis; SEP; apoptotic;
KW surface receptor; TRAIL protein.
XX
OS Homo sapiens.
XX
PN FR2766713-A1.
XX
PD 05-FEB-1999.
XX
PF 04-AUG-1997; 97FR-00010176.
XX
PR 04-AUG-1997; 97FR-00010176.
XX
PA (INNR) BIO MERIEUX.
XX
PI Rieger F, Belliveau JF, Perron H;
XX
DR WPI; 1999-156177/14.
XX
PT Use of polypeptide derived from TRAIL protein for diagnosis of
PT degenerative disease - autoimmunity and inflammation, also useful in
PT prevention or treatment, and similar use of corresponding ligand and
PT nucleic acid.

XX Claim 2; Page 13; 21pp; French.
XX
CC The specification describes the use a polypeptide corresponding to at
CC least the primary sequence of part of the present sequence to produce a
CC diagnostic, prophylactic or therapeutic composition useful in cases of
CC degenerative, autoimmune and inflammatory diseases. The polypeptides can
CC be used in treatment of neurodegenerative diseases, lupus erythematosus,
CC rheumatoid arthritis, and SEP. The polypeptides are apoptotic in central
CC nervous system cells, antigenic and specifically recognise the surface
CC receptor of the TRAIL protein. The polypeptide is a marker of disease and
CC a therapeutic target, e.g. its apoptotic activity can be blocked with an
CC anti-TRAIL antibody or a TRAIL equivalent that binds to specific
CC receptors, inhibiting formation of natural complex
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 2; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMDKYSGKGIACFLKEDDSYWDNDDESNPCQVQKWLRLVVKMLRTSEE 60
DB 39 TNELKQMDKYSGKGIACFLKEDDSYWDNDDESNPCQVQKWLRLVVKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVIEHKGFIYYSQTYFRFOEIKENTKNDKQVQYIYKITSYD 180
DB 159 SGHSFSLNHLRNGELVIEHKGFIYYSQTYFRFOEIKENTKNDKQVQYIYKITSYD 218
QY 181 PILLMKSARNCSWKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNCSWKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 10
AAY27012
ID AAY27012 standard; protein; 281 AA.
XX
AC AAY27012;
XX
DT 24-SEP-1999 (first entry)
XX
DE Human Apo-2 ligand (Apo-2L) polypeptide.
XX
KW Cytokine; Apo-2 ligand; Apo-2L; apoptosis; cancer; autoimmune disorder;
KW lupus; immune-mediated glomerular nephritis; human.
XX
OS Homo sapiens.
XX
PN WO9936535-A1.
XX
PD 22-JUL-1999.
XX
PF 15-JAN-1999; 99WO-US0001039.
XX
PR 15-JAN-1998; 98US-00007886.
PR 15-APR-1998; 98US-00060533.
XX
PA (GETH) GENENTECH INC.
XX
PI Ashkenazi AJ, Kelley RF, O'connel MT, Pitti RM, Schwall RH;
XX
DR WPI; 1999-444397/37.
DR N-PSDB; AAX86987.
XX

PT A novel cytokine, designated Apo-2 ligand, useful for inducing apoptosis
 PT in mammalian cancer cells.
 XX
 XX Claim 1; Fig 1A; 86pp; English.

CC This sequence represents a novel human cytokine, designated Apo-2 ligand
 CC (Apo-2L). The Apo-2L polypeptide can be produced by standard recombinant
 CC methodology. Apo-2L is useful for inducing apoptosis in mammalian cancer
 CC cells. This is useful for the treatment of cancer. Apo-2L can be used to
 CC induce apoptosis for pathological conditions characterized by decreased
 CC levels of apoptosis, e.g. autoimmune disorders like lupus and immune-
 CC mediated glomerular nephritis and cancer. Apo-2L and its nucleic acid
 CC coding sequence can also be used in quantitative and screening diagnostic
 CC techniques. Anti-Apo-2L antibodies can be used for treating diseases
 CC associated with increased apoptosis
 XX
 XX Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 2; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYSKSGIACFLKEDDSYDNDDESNMPCQVQWQLRQLVRKMLRTSEE 60
 DB 39 TNELKQMDKYSKSGIACFLKEDDSYDNDDESNMPCQVQWQLRQLVRKMLRTSEE 98
 QY 61 TISTVQEKQNIISPLVRERGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
 DB 99 TISTVQEKQNIISPLVRERGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFLSNLHRLNGELVIEHKGFYIYSQTYFRFQEEIKENTKNDKQWQVIYKYTSYD 180
 DB 159 SGHSFLSNLHRLNGELVIEHKGFYIYSQTYFRFQEEIKENTKNDKQWQVIYKYTSYD 218
 QY 181 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 DB 279 LVG 281

RESULT 11
 AAY81956
 ID AAY81956 standard; protein; 281 AA.
 XX
 XX AAY81956;
 XX
 XX 10-JUL-2000 (first entry)
 XX
 XX Human Apo-2 ligand protein sequence.
 XX
 XX Apo-2 ligand; human; monoclonal antibody; hybridoma cell line; diagnosis;
 XX therapy; apoptosis; cancer.
 XX
 XX Homo sapiens.
 XX
 XX US6046048-A.
 XX
 XX 04-APR-2000.
 XX
 XX 08-JAN-1997; 97US-00780496.
 XX
 XX 09-JAN-1996; 96US-0009755P.
 XX
 XX (GENTH) GENENTECH INC.
 XX
 XX Kim KJ, Ashkenazi AJ, Chuntharapai A;
 XX WPI; 2000-282690/24.
 XX N-PSDB; AAA07425.
 XX

PT New isolated monoclonal antibodies having antigen specificity for Apo-2
 PT ligand, e.g. 206, 2E11 or 5C2, useful for detecting the expression of Apo
 PT -2 ligand serum, and for treating diseases associated with increased
 PT apoptosis.
 XX
 XX Claim 9; Fig 1a; 46pp; English.

CC This sequence is the human Apo-2 ligand protein, which is recognised by
 CC monoclonal antibodies produced by the hybridoma cell lines of the
 CC invention. The hybridoma cell lines are deposited under the American Type
 CC Culture Collection Accession Numbers: ATCC HB-12256, HB-12257, HB-12258
 CC and HB-12259. The Apo-2 ligand antibodies may be used in diagnostic
 CC assays for Apo-2 ligand, e.g. detecting its expression in specific cells,
 CC tissues, or serum. The antibodies may also be employed as therapeutics.
 CC For instance, anti-Apo-2 ligand antibodies which block Apo-2 ligand
 CC activity, like Apo-2 ligand-induced apoptosis, may be employed to treat
 CC pathological conditions or diseases associated with increased apoptosis.
 CC They are also useful for the affinity purification of Apo-2 ligand from
 CC recombinant cell culture or natural sources. The Apo-2 ligand itself may
 CC be used to treat diseases e.g. cancer, by inducing apoptosis in cells
 CC
 XX Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYSKSGIACFLKEDDSYDNDDESNMPCQVQWQLRQLVRKMLRTSEE 60
 DB 39 TNELKQMDKYSKSGIACFLKEDDSYDNDDESNMPCQVQWQLRQLVRKMLRTSEE 98
 QY 61 TISTVQEKQNIISPLVRERGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
 DB 99 TISTVQEKQNIISPLVRERGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFLSNLHRLNGELVIEHKGFYIYSQTYFRFQEEIKENTKNDKQWQVIYKYTSYD 180
 DB 159 SGHSFLSNLHRLNGELVIEHKGFYIYSQTYFRFQEEIKENTKNDKQWQVIYKYTSYD 218
 QY 181 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKSARNSCWSKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 DB 279 LVG 281

RESULT 12
 AAB24038
 ID AAB24038 standard; protein; 281 AA.
 XX
 XX AAB24038;
 XX
 XX 25-JAN-2001 (first entry)
 XX
 XX Human PRO1096 protein sequence SEQ ID NO:51.
 XX
 XX Human; tumour; diagnosis; neoplastic disease; proliferation; cancer;
 XX identification; tumorigenesis; anticancer; detection.
 XX
 XX Homo sapiens.
 XX
 XX WO200053750-A1.
 XX
 XX 14-SEP-2000.
 XX
 XX 02-DEC-1999; 99WO-US028551.
 XX
 XX 08-MAR-1999; 99WO-US005028.
 XX
 XX 01-SEP-1999; 99WO-US020111.
 XX
 XX 29-OCT-1999; 99US-0162506P.
 XX
 XX 30-NOV-1999; 99WO-US028313.
 XX

PR 01-DEC-1999; 99WO-US028634.
 XX (GETH) GENENTECH INC.
 PA Botstein D, Goddard A, Gurney AL, Roy MA, Watanabe CK, Wood WI;
 XX N-PSDB; AAC58120.
 DR WPI; 2000-594320/56.
 XX N-PSDB; AAC58120.
 XX Antibodies specific for PRO polypeptides, used to diagnose and inhibit
 PT the growth of tumors in mammals, and to identify inhibitors of PRO
 PT polypeptide activity or expression.
 XX Claim 61; Fig 36; 226pp; English.
 XX The present invention describes an antibody that binds to a human protein
 CC (I) selected from: PRO381; PRO1269; PRO1410; PRO1755; PRO1780; PRO3434;
 CC PRO1927; PRO3567; PRO1295; PRO1293; PRO1303; PRO4344; PRO4354; PRO4397;
 CC PRO4407; PRO1555; PRO1036; and PRO2262. (I) has anticancer
 CC activity and can be used to diagnose tumors in mammals, by detecting
 CC complex formation when the antibody is contacted with test cells.
 CC Increased expression of genes encoding (I) can also be detected to
 CC diagnose tumors. Agents which inhibit the activity of (I), especially
 CC the antibodies, or an antisense oligonucleotide which hybridizes to genes
 CC encoding (I), can be used to inhibit tumour growth, preferably by
 CC inducing cell death. Methods from the present invention can be used to
 CC identify compounds which inhibit the biological activity of (I). AAC58019
 CC to AAC58102 represent PCR primers and hybridisation probes used in
 CC examples from the present invention for human PRO sequences. AAC58103 to
 CC AAC58122 and AAC24021 to AAC24040 represent human PRO polynucleotide and
 CC protein sequences given in the exemplification of the present invention
 XX Sequence 281 AA;
 SQ

Query Match 100.0%; Score 1287; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TNELKQMDKYSGSGIACFLKEDDSYDNDSESNPCQVQKQRLVRLKMLRTSEE 60
 Db 39 TNELKQMDKYSGSGIACFLKEDDSYDNDSESNPCQVQKQRLVRLKMLRTSEE 98
 Qy 61 TISTVQEKQNIISPLVREGRGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
 Db 99 TISTVQEKQNIISPLVREGRGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
 Qy 121 SGHSFLSNLHRLNGELVIEHKGFPYIYSQTYFRFQBEIKENTKDKQVQYIYKTSYDP 180
 Db 159 SGHSFLSNLHRLNGELVIEHKGFPYIYSQTYFRFQBEIKENTKDKQVQYIYKTSYDP 218
 Qy 181 PILLKMSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 Db 219 PILLKMSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 Qy 241 LVG 243
 Db 279 LVG 281

RESULT 13
 AAB08545
 ID AAB08545 standard; protein; 281 AA.
 XX AC AAB08545;
 XX 20-DEC-2000 (first entry)
 XX Amino acid sequence of a human TRAIL polypeptide.
 XX Human; TRAIL; tumour necrosis factor; TNF; diterpenoid triepoxide;
 KW TNF related apoptosis-inducing ligand; tumour cell;
 KW TRAIL receptor ligand; solid tumour; carcinoma; mammary carcinoma;
 KW non-small cell lung carcinoma.

XX Homo sapiens.
 OS WO200048619-A1.
 PN 24-AUG-2000.
 XX 15-FEB-2000; 2000WO-US003891.
 XX 16-FEB-1999; 99US-0120313P.
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 PA Rosen GD;
 XX WPI; 2000-558253/51.
 DR N-PSDB; AAA64325.
 XX Killing of tumor cells, e.g. solid tumors or carcinoma, comprises
 PT administration of synergistic combination of diterpenoid diepoxide and
 PT tumor necrosis factor related apoptosis-inducing ligand.
 XX Disclosure; Page 23-24; 29pp; English.
 XX The present sequence represents a human TRAIL (tumour necrosis factor
 CC (TNF) related apoptosis-inducing ligand) polypeptide. The specification
 CC describes a method for enhanced killing of tumour cells. The method
 CC comprises contacting a susceptible tumour cell with a synergistic mixture
 CC of a TRAIL receptor ligand and a diterpenoid triepoxide in a combined
 CC dosage to kill at least 50 % of the cells. This mixture is synergistic,
 CC and so is active at lower doses and against otherwise resistant cell
 CC lines. The method is used for killing tumour cells, especially solid
 CC tumours or carcinomas (especially mammary carcinoma or non-small cell
 CC lung carcinoma)
 XX Sequence 281 AA;
 SQ

Query Match 100.0%; Score 1287; DB 3; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TNELKQMDKYSGSGIACFLKEDDSYDNDSESNPCQVQKQRLVRLKMLRTSEE 60
 Db 39 TNELKQMDKYSGSGIACFLKEDDSYDNDSESNPCQVQKQRLVRLKMLRTSEE 98
 Qy 61 TISTVQEKQNIISPLVREGRGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
 Db 99 TISTVQEKQNIISPLVREGRGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
 Qy 121 SGHSFLSNLHRLNGELVIEHKGFPYIYSQTYFRFQBEIKENTKDKQVQYIYKTSYDP 180
 Db 159 SGHSFLSNLHRLNGELVIEHKGFPYIYSQTYFRFQBEIKENTKDKQVQYIYKTSYDP 218
 Qy 181 PILLKMSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 Db 219 PILLKMSARNSCWSKDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 Qy 241 LVG 243
 Db 279 LVG 281

RESULT 14
 AAB28691
 ID AAB28691 standard; protein; 281 AA.
 XX AC AAB28691;
 XX 14-FEB-2001 (first entry)
 XX Human AGP-1.
 XX Human; AGP-1; type II transmembrane protein; cytostatic; antiviral;

KW antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV;
KW human immunodeficiency virus; apoptosis; proliferative disorder; cancer;
KW hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder;
KW transplant rejection; cardiovascular disease; arteriosclerosis.
XX Homo sapiens.
XX WO200063253-A1.
XX PD 26-OCT-2000.
XX 24-MAR-2000; 2000WO-US008004.
XX PR 16-APR-1999; 99US-00293245.
XX PA (AMGE-) AMGEN INC.
XX PI Hsu H, Meng S;
XX DR WPI; 2000-565240/64.
XX DR N-PSDB; AAC67831.
XX Fusion protein of AGP-1 protein and an Fc region, used to treat
PT proliferative disorders, immune disorders, and virally-induced disorders.
XX Claim 3; Fig 2; 93pp; English.
XX The present sequence is human AGP-1, a type II transmembrane protein.
CC Fusion proteins comprising an Fc immunoglobulin region fused to the N-
CC terminal portion of the AGP-1 protein have been produced. The fusion
CC proteins can be used to induce apoptosis in a tissue, and to treat
CC proliferative disorders, immune disorders, or virally-induced disorders.
CC The proliferative disorders include cancers, such as breast, prostate,
CC lung or colon cancer. The viral infections include hepatitis, and
CC acquired immunodeficiency syndrome (AIDS), and the immune disorders may
CC be autoimmune disorders or transplant rejection. Cardiovascular diseases
CC such as arteriosclerosis may also be treated. The AGP-1 containing fusion
CC proteins have increased biological activity compared to the soluble AGP-1
CC proteins used in prior art therapies
XX Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDNDDEESMNSPCQVQWQLRQVRLVRLTSEE 60
Db 39 TNELKQMDKYSKSGIACFLKEDDSYWDNDDEESMNSPCQVQWQLRQVRLVRLTSEE 98
QY 61 TISTVQEKQONISPLVRERGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQONISPLVRERGPQVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVIEHKGPIYYSOTYFRFOEIEKENTKNDKQVQYIKYTSYPD 180
Db 159 SGHSFLSNLHRLNGELVIEHKGPIYYSOTYFRFOEIEKENTKNDKQVQYIKYTSYPD 218
QY 181 PILLMKSARNCSWSDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFQAF 240
Db 219 PILLMKSARNCSWSDAEYGLYSIYOGGIFELKENDRIFVSVTNEHLIDMDHEASFFQAF 278
QY 241 LVG 243
Db 279 LVG 281

RESULT 15
AAB50977
ID AAB50977 standard; protein; 281 AA.
XX
AC AAB50977;
XX

DT 21-MAR-2001 (first entry)
XX Human PRO1096 protein.
XX Human; PRO; cytostatic; nootropic; neuroprotective; respiratory general;
KW antiinflammatory; antiangiogenic; immunosuppressive; immunostimulant;
KW PRO agonist; cancer; inflammatory disorder; immunological disorder.
XX Homo sapiens.
XX WO200073348-A2.
XX PD 07-DEC-2000.
XX 30-MAY-2000; 2000WO-US014941.
XX 02-JUN-1999; 99WO-US012252.
XX 22-JUN-1999; 99US-0140650P.
XX 23-JUN-1999; 99US-0141037P.
XX 21-JUL-1999; 99US-0144758P.
XX 01-SEP-1999; 99WO-US020111.
XX 08-SEP-1999; 99WO-US020594.
XX 29-OCT-1999; 99US-0162506P.
XX 30-NOV-1999; 99WO-US028313.
XX 01-DEC-1999; 99WO-US028634.
XX 02-DEC-1999; 99US-02028551.
XX 09-DEC-1999; 99US-0170262P.
XX 16-DEC-1999; 99WO-US030095.
XX 20-DEC-1999; 99WO-US030999.
XX 06-JAN-2000; 2000WO-US000376.
XX 11-FEB-2000; 2000WO-US003565.
XX 18-FEB-2000; 2000WO-US004341.
XX 18-FEB-2000; 2000WO-US004342.
XX 02-MAR-2000; 2000WO-US005841.
XX 03-MAR-2000; 2000US-0187202P.
XX 10-MAR-2000; 2000WO-US008319.
XX 15-MAR-2000; 2000WO-US008884.
XX 30-MAR-2000; 2000WO-US008439.
XX 17-MAY-2000; 2000WO-US013705.
XX (GETH) GENENTECH INC.
XX Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
PI Shelton DL, Smith V, Watanabe CK, Wood WI;
XX WPI; 2001-016509/02.
XX N-PSDB; AAC91579.

Twenty eight nucleic acids encoding PRO polypeptides which are useful for
treating various tumors, e.g. breast cancer, and other inflammatory,
angiogenic and immunological disorders.

Claim 31; Fig 54; 188pp; English.

The present sequence is one of twenty eight novel PRO polypeptides. The
PRO polypeptides and their agonists, including antibodies, peptides, and
small molecule agonists, may be used to treat various tumors e.g.,
cancers such as breast cancer, ovarian cancer, renal cancer, colorectal
cancer, uterine cancer, prostate cancer, lung cancer, bladder cancer,
central nervous system cancer, melanoma or leukaemia. They are also
useful for treating other disorders such as neuronal, glial, astrocytal,
hypothalamic and other glandular, macrophagal, epithelial, stromal and
blastocoeic disorders, and inflammatory, angiogenic and immunological
disorders

Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDNDDEESMNSPCQVQWQLRQVRLVRLTSEE 60
|||||

Db 39 TNELQKQDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQKQLRVKQMLRTSEE 98
 QY 61 TISTVQEKQONISPLVRERGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120
 Db 99 TISTVQEKQONISPLVRERGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFLSNLHLRNGELVIEHKGFFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYD 180
 Db 159 SGHSFLSNLHLRNGELVIEHKGFFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYD 218
 QY 181 PILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF 240
 Db 219 PILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF 278
 QY 241 LVG 243
 Db 279 LVG 281

RESULT 16

AAB67243
 ID AAB67243 standard; protein; 281 AA.

AC AAB67243;

DT 18-APR-2001 (first entry)

DE Human Apo2 ligand.

KW Human; Apo2 ligand: divalent metal ions; viral infection; cancer.

OS Homo sapiens.

PN WO200100832-A1.

XX 04-JAN-2001.

PF 26-JUN-2000; 2000WO-US017579.

PR 28-JUN-1999; 99US-0141342P.

XX (GETH) GENENTECH INC.

PI Ashkenazi AJ, Hymowitz S, Kelley RF, Koumenis I, Leung S;

PI O'connell M, Pai R, Shahrokh Z, Simmons L;

XX WPI; 2001-123012/13.

XX Use of divalent metal ions for making Apo-2 ligand and in formulations containing Apo-2 ligand for increasing yield and stability of ligand trimers, useful for therapeutic applications.

XX Claim 6; Fig 1; 60pp; English.

XX The present invention relates to a formulation comprising Apo-2 ligand and divalent metal ions. Apo-2 ligand and the formulation are useful for treating cancers and viral infections. Addition of divalent metal ions for making Apo-2 ligand and formulations containing Apo-2 ligand results in increased yield and stability of Apo-2 ligand trimers

XX Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 4; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELQKQDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQKQLRVKQMLRTSEE 60

Db 39 TNELQKQDKYKSGIACFLKEDDSYWDPNDEESMNSPCQVQKQLRVKQMLRTSEE 98

QY 61 TISTVQEKQONISPLVRERGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 120

Db 99 TISTVQEKQONISPLVRERGPORVAAHITGTRGRNTLSSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFLSNLHLRNGELVIEHKGFFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYD 180
 Db 159 SGHSFLSNLHLRNGELVIEHKGFFYYISQTYFRFOEIKENTKNDKQMVQIYKYTSYD 218
 QY 181 PILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF 240
 Db 219 PILLMKSARNCSWCKDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF 278
 QY 241 LVG 243
 Db 279 LVG 281

RESULT 17

AAE11031

ID AAE11031 standard; protein; 281 AA.

XX AAE11031;

DT 18-DEC-2001 (first entry)

DE Human TNF related apoptosis inducing ligand (TRAIL) protein.

KW Human; tumour necrosis factor; TNF; cytokine; cytostatic; virucide;
 KW TNF related apoptosis inducing ligand; TRAIL; cancer; viral infection;
 KW human immunodeficiency virus; HIV; leukaemia; gene therapy; lymphoma;
 melanoma.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Domain 1..18

FT FT /label= N_terminal_cytoplasmic_domain

FT Region 19..38

FT FT /label= Transmembrane_region

FT Domain 39..281

FT FT /label= Extracellular_domain

XX US6284236-B1.

XX 04-SEP-2001.

XX 26-MAY-1999; 99US-00320424.

XX 29-JUN-1995; 95US-00496632.

XX 01-NOV-1995; 95US-00548368.

XX 25-JUN-1996; 96US-00670354.

XX 26-MAR-1998; 98US-00048641.

XX 10-NOV-1998; 98US-00190046.

XX (IMMV) IMMUNEX CORP.

XX Wiley SR, Goodwin RG;

XX WPI; 2001-595463/67.

XX N-ESDB; AAD18395.

XX New tumor necrosis factor related apoptosis inducing ligand polypeptides for treating viral infections (e.g. bovine viral diarrhoea or human immunodeficiency virus), or cancers (e.g. leukemia or lymphoma).

XX Claim 2; Col 45-48; 41pp; English.

XX The invention relates to a cytokine designated as tumour necrosis factor (TNF) related apoptosis inducing ligand (TRAIL), which induces apoptosis of certain target cells, including cancer cells and virally infected cells. The TRAIL polypeptides are useful in killing cancer cells, in treating viral infections (e.g. bovine viral diarrhoea or human immunodeficiency virus (HIV)) and cancers (e.g. leukaemia, lymphoma and melanoma), as a research reagent useful in studying apoptosis including the regulation of programmed cell death. TRAIL DNA sequences may be employed in developing a gene therapy approach to treating disorders

CC mediated by defective or insufficient amounts of TRAIL, in the production
CC of TRAIL polypeptides and as probes or primers in polymerase chain
CC reactions (PCR). The present sequence is human TRAIL protein
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDESNPCWQVKQLRQLVKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDESNPCWQVKQLRQLVKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPQVAHAHTGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGPQVAHAHTGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFOBEIKENTKNDKQWQYIYKTSYDP 180
DB 159 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFOBEIKENTKNDKQWQYIYKTSYDP 218
QY 181 PILLMKSARNSCWSDAEGYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNSCWSDAEGYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 18
AAB48350
ID AAB48350 standard; protein; 281 AA.
XX
AC AAB48350;
XX
DT 20-APR-2001 (first entry)
XX
DE Human TL2 polypeptide.
XX
KW Tumour necrosis factor; TNF; TNF related receptor; TR6; human; TL2;
KW anti-inflammatory; immunosuppressive; cerebroprotective; vasotropic;
KW antiasthmatic; anti-HIV; osteopathic; cytostatic; antiatherosclerotic;
KW neurotropic; neuroprotective; antiarthritic; antirheumatic; antischismic;
KW gene therapy; vaccine; TNF-alpha; bone disease; cancer; TRAIL.
XX
OS Homo sapiens.
XX
PN WO200077191-A1.
XX
PD 21-DEC-2000.
XX
PF 12-JUN-2000; 2000WO-US016134.
XX
PR 15-JUN-1999; 98US-00333593.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Deen KC, Young PR, Marshall LA, Roshak AK, Tan KB, Truneh A;
XX
DR WPI; 2001-112223/12.
DR N-PSDB; AAC84745.
XX
PT New tumor necrosis factor related receptor TR6 polynucleotides and
PT polypeptides useful for e.g. for treating chronic and acute inflammation,
PT arthritis, septicemia, autoimmune diseases, infection, cancer, bone
PT diseases.
XX
PS Disclosure; Page 26; 47pp; English.
XX
CC The invention relates to a human tumour necrosis factor (TNF) related
CC receptor, TR6. TR6 can be expressed by standard recombinant methodology.

CC The TR6 polypeptides are useful for treating chronic and acute
CC inflammation, rheumatoid arthritis, septicemia, autoimmune diseases (e.g.
CC inflammatory bowel disease, psoriasis), transplant rejection, graft vs.
CC host disease, infection, stroke, ischaemia, acute respiratory disease
CC syndrome, asthma, restenosis, brain injury, AIDS, bone diseases, cancer,
CC atherosclerosis, and Alzheimer's disease. These may also be used to
CC inhibit production of TNF-alpha and eicosanoids, as research reagents and
CC materials for discovering treatments and diagnostics to animal and human
CC diseases. The polypeptides may further be used as immunogens to produce
CC antibodies immunospecific for the TR6 polypeptides. The polynucleotides
CC may also be used as hybridization probes for cDNA and genomic DNA, for
CC isolating full-length cDNAs and genomic clones encoding TR6 and of other
CC genes having high sequence similarity to TR6 gene, and for chromosome
CC identification. The present sequence represents a human TL2 polypeptide.
CC TL2 is also known as TRAIL (TNF-related apoptosis-inducing ligand) and is
CC a ligand for the TL2 polypeptide
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDESNPCWQVKQLRQLVKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDESNPCWQVKQLRQLVKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGPQVAHAHTGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGPQVAHAHTGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFOBEIKENTKNDKQWQYIYKTSYDP 180
DB 159 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRFOBEIKENTKNDKQWQYIYKTSYDP 218
QY 181 PILLMKSARNSCWSDAEGYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNSCWSDAEGYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 19
ABB08133
ID ABB08133 standard; protein; 281 AA.
XX
AC ABB08133;
XX
DT 10-SEP-2002 (first entry)
XX
DE Human TRAIL polypeptide.
XX
KW Dendritic cell; mobilisation factor; T cell; adjuvant; antibacterial;
KW fungicide; protozoicide; virucide; anti-inflammatory; anti-HIV;
KW tuberculostatic; cytostatic; human; TRAIL.
XX
OS Homo sapiens.
XX
PN WO200236141-A2.
XX
PD 10-MAY-2002.
XX
PF 30-OCT-2001; 2001WO-US044834.
XX
PR 02-NOV-2000; 2000US-0245721P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Lynch DH, De Smedt TN, Maliszewski CR, Butz EA, Miller RE;
PI Thomas EK;
XX

DR WPI; 2002-500114/53.
 XX Treating an individual suffering from infection, e.g. inflammation,
 PT chickenpox or AIDS, by administering a combination of dendritic cell
 PT mobilization factor or maturation agent, T cell enhancing factor and
 PT antigen-specific T cells.
 XX
 XX
 PS Disclosure; Page 40-42; 43pp; English.
 XX
 CC The invention relates to treating an individual at risk for or suffering
 CC from infection with a pathogenic or opportunistic organism. The method
 CC involves administering a combination of two to five agents comprising:
 CC (a) dendritic cell mobilisation factor; (b) dendritic cell maturation
 CC agent; (c) dendritic cell activation agent; (d) T cell enhancing factor;
 CC or (e) activated, antigen-specific T cells. The methods are useful for
 CC treating an individual at risk for or suffering from infection with a
 CC pathogenic or opportunistic organism, e.g. viruses (e.g. HIV), bacteria
 CC (e.g. M. tuberculosis), yeast, fungi (e.g. C. albicans) or protozoa (e.g.
 CC T. cruzi, which causes Chaga's disease). The methods are especially
 CC useful for treating an individual suffering from immunosuppression by
 CC enhancing a lymphocyte-mediated immune response. In particular, the
 CC method is useful for treating inflammations, chickenpox, oral or genital
 CC herpes, mononucleosis, multifocal leukoencephalopathy, hepatitis, AIDS, T
 CC cell leukemia or T cell lymphoma. The activated antigen-presenting
 CC dendritic cells are useful as a vaccine adjuvant. The present sequence
 CC represents a human TRAIL polypeptide fragment
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 1287; DB 5; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELQWQMDKYSKSGIACFLKEDDSYDNDDEESNPSNCKEALGRKINSWESSR 60
 DB 39 TNELQWQMDKYSKSGIACFLKEDDSYDNDDEESNPSNCKEALGRKINSWESSR 98
 QY 61 TISTVQEQKQNTISPLVRERGPQVAAHITGTRGRSNTLSSPNSNCKEALGRKINSWESSR 120
 DB 99 TISTVQEQKQNTISPLVRERGPQVAAHITGTRGRSNTLSSPNSNCKEALGRKINSWESSR 158
 QY 121 SGHSLNHLNRLNGELVHEKGFYIYSQTYFRFOEIKENTKDKQWQVYIKYTSYD 180
 DB 159 SGHSLNHLNRLNGELVHEKGFYIYSQTYFRFOEIKENTKDKQWQVYIKYTSYD 218
 QY 181 PILLMKSARNSCWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKSARNSCWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 RESULT 20
 ASG31630
 ID ASG31630 standard; protein; 281 AA.
 XX
 AC ASG31630;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 DE Human TRAIL protein.
 XX
 KW Tumour; cancer; dendritic cell mobilisation factor; tumour-killing agent;
 KW dendritic cell maturation agent; T cell enhancing factor; skin cancer;
 KW antigen-specific T cell; prostate cancer; liver cancer; bone tumour;
 KW brain tumour; spinal cord tumour; cervical intraepithelial neoplasia;
 KW actinic keratosis; dendritic cell maturation stimulator; cytostatic;
 KW dendritic cell activator; T cell enhancer; human; TRAIL.
 XX
 OS Homo sapiens.
 XX

PN WO200266044-A2.
 XX
 PD 29-AUG-2002.
 XX
 PF 23-OCT-2001; 2001WO-US046254.
 XX
 PR 24-OCT-2000; 2000US-0242868P.
 XX
 PA (IMMUNEX) IMMUNEX CORP.
 XX
 XX Thomas EK, Lyman SD, Lynch DH, De Smedt TN, Maliszewski CR;
 XX WPI; 2002-674891/72.
 XX
 PT Treating an individual with tumors or cancers, e.g. liver cancer or brain
 PT tumor, by administering a combination of dendritic cell populations, T
 PT cell enhancing factors and activated, antigen-specific T cells.
 XX
 PS Disclosure; Page 41-43; 44pp; English.
 XX
 CC The present invention relates to a new method for treating a tumour-
 CC bearing subject. The method involves administering a combination of 2 to
 CC 5 agents comprising dendritic cell mobilisation factor, dendritic cell
 CC maturation agent, tumour-killing agent, T cell enhancing factor or
 CC activated, antigen-specific T cells. The method is useful for treating
 CC tumours or cancers in a subject e.g. skin cancer, prostate cancer, liver
 CC cancer, tumours of the bone, brain or spinal cord, actinic keratosis, or
 CC cervical intraepithelial neoplasia. The present amino acid sequence
 CC represents the human TRAIL protein that was used in the method of the
 CC invention
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 1287; DB 5; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELQWQMDKYSKSGIACFLKEDDSYDNDDEESNPSNCKEALGRKINSWESSR 60
 DB 39 TNELQWQMDKYSKSGIACFLKEDDSYDNDDEESNPSNCKEALGRKINSWESSR 98
 QY 61 TISTVQEQKQNTISPLVRERGPQVAAHITGTRGRSNTLSSPNSNCKEALGRKINSWESSR 120
 DB 99 TISTVQEQKQNTISPLVRERGPQVAAHITGTRGRSNTLSSPNSNCKEALGRKINSWESSR 158
 QY 121 SGHSLNHLNRLNGELVHEKGFYIYSQTYFRFOEIKENTKDKQWQVYIKYTSYD 180
 DB 159 SGHSLNHLNRLNGELVHEKGFYIYSQTYFRFOEIKENTKDKQWQVYIKYTSYD 218
 QY 181 PILLMKSARNSCWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKSARNSCWSDAEYGLYSIYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 RESULT 21
 AAU75062
 ID AAU75062 standard; protein; 281 AA.
 XX
 AC AAU75062;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Human TNF related apoptosis inducing ligand (TRAIL) protein.
 XX
 KW TRAIL; TNF; apoptosis; tumour; death domain receptor ligand;
 KW diterpeneoid triepoxide; cytostatic activity; C-LAP2; C-LAP1; carcinoma;
 KW mammary adenocarcinoma; non-small cell lung carcinoma;
 KW neurological malignancy; haematological malignancy; lichen planus;
 KW non-Hodgkin's lymphoma; chronic lymphocytic leukaemia; anti-angiogenic;

KW malignant cutaneous T-cell; lymphomatoid papulosis; anti-metastatic;
 KW non-MF cutaneous T-cell lymphoma; mycosis fungoides; anti-tumour;
 KW T-cell rich cutaneous lymphoid hyperplasia; bullous pemphigoid;
 KW discoid lupus erythematosus; human.
 XX Homo sapiens.
 XX US6329148-B1.
 XX 11-DEC-2001.
 XX 15-FEB-2000; 2000US-00505250.
 XX 16-FEB-1999; 99US-0120313P.
 XX 20-AUG-1999; 99US-0149989P.
 XX (STRD) UNIV LELAND STANFORD JUNIOR.
 XX Rosen GD, Kao P;
 XX WPI; 2002-121125/16.
 XX N-PSDB; ABK13132.
 XX Use of a synergistic combination of death domain receptor ligands and
 PT diterpenoid triepoxides for killing of tumor cells.
 XX Disclosure; Col 17-20; 20pp; English.
 XX This invention relates to a novel method for enhanced killing of tumor
 CC cells comprising contacting a tumor cell with a synergistic combination
 CC of a death domain receptor ligand and a diterpenoid triepoxide. This
 CC method has cytostatic activity and works by blocking TNF-alpha mediated
 CC induction of c-IAP2 and c-IAP1. The method of the invention may be used
 CC for treating tumors, particularly solid tumors, e.g. carcinoma, mammary
 CC adenocarcinoma and non-small cell lung carcinoma also neurological
 CC malignancies, haematological malignancies, e.g. non-Hodgkin's lymphoma,
 CC chronic lymphocytic leukaemia, malignant cutaneous T-cells, mycosis
 CC fungoides, non-MF cutaneous T-cell lymphoma, lymphomatoid papulosis, T-
 CC cell rich cutaneous lymphoid hyperplasia, bullous pemphigoid, discoid
 CC lupus erythematosus, lichen planus. The combination may be administered
 CC with other active agents, e.g. anti-metastatic, anti-tumour or anti-
 CC angiogenic agents. The potent synergy between the diterpenoids and the
 CC death domain ligands allows increased killing at equivalent or lower
 CC doses, and can sensitize otherwise resistant cells. This sequence
 CC represents the human TNF related apoptosis inducing ligand (TRAIL)
 CC protein sequence. TRAIL is a death domain receptor used in the used
 CC method of the invention in combination with diterpenoid triepoxides to
 CC kill tumors by induction of apoptosis
 XX
 XX Sequence 281 AA;
 Query Match 100.0%; Score 1287; DB 5; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYKSGIACFLKEDDSYNDPDEENSMNSPCQVQKQLRQVVKMLRTSEE 60
 DB 39 TNELKQMDKYKSGIACFLKEDDSYNDPDEENSMNSPCQVQKQLRQVVKMLRTSEE 98
 QY 61 TISTVQEKQNIISPLVREERGFQVAAHITCTGRSNTLSPNSKNEKALGRKINSWESSR 120
 DB 99 TISTVQEKQNIISPLVREERGFQVAAHITCTGRSNTLSPNSKNEKALGRKINSWESSR 158
 QY 121 SGHSFLNLHRLNGELVTHKGFYIYSQYFESFOBEIKENTKNDKQVYIKYTSYD 180
 DB 159 SGHSFLNLHRLNGELVTHKGFYIYSQYFESFOBEIKENTKNDKQVYIKYTSYD 218
 QY 181 PILLMKARSNCWSKDAEYGLISTYQGIIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 DB 219 PILLMKARSNCWSKDAEYGLISTYQGIIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 QY 241 LVG 243
 DB 39 TNELKQMDKYKSGIACFLKEDDSYNDPDEENSMNSPCQVQKQLRQVVKMLRTSEE 98

Db 279 LVG 281
 RESULT 22
 AAMS1077
 ID AAMS1077 standard; protein; 281 AA.
 XX AAMS1077;
 AC AAMS1077;
 XX 30-MAY-2002 (first entry)
 DT Human Apo-2 ligand (TRAIL).
 XX Apo-2 ligand; Apo-2L; TRAIL; human; apoptosis; colorectal cancer; tumour;
 KW antitumour; therapy.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Protein 114..281
 FT /note= "Apo-2L polypeptide used in method of Claim 18"
 FT
 XX WO200209755-A2.
 PN 07-FEB-2002.
 XX 27-JUL-2001; 2001WO-US023691.
 PF 27-JUL-2000; 2000US-0221256P.
 PR (GETH) GENENTECH INC.
 XX Escandon E, Fox JA, Kelley SK, Xiang H;
 PI WPI; 2002-268997/31.
 DR Use of CPT-11 which is a chemotherapeutic agent of the topoisomerase I
 XX inhibitor class, and Apo-2 ligand receptor agonist for enhancing
 PT apoptosis in mammalian cells, or for treating cancer in a mammal.
 XX Claim 18; Page 79-80; 84pp; English.
 PS The present sequence is that of human Apo-2 ligand (Apo-2L or TRAIL). The
 CC invention relates to methods of inducing apoptosis in mammalian cells,
 CC and especially to the use of Apo-2L receptor agonists and CPT-11 (a
 CC chemotherapeutic agent of the topoisomerase I inhibitor class) to
 CC synergistically induce apoptosis in mammalian cells, in particular
 CC mammalian cancer cells, and especially colorectal cancer cells (Claimed).
 CC The cells may be in cell culture or in a mammal, e.g. a mammal suffering
 CC from cancer or a condition in which induction of apoptosis in the cells
 CC is desirable. A claimed method of treating cancer in a mammal comprises
 CC administering CPT-11 and Apo-2L receptor agonist, where the CPT-11 is
 CC administered about 6-72 hours prior to administration of the Apo-2L
 CC receptor agonist. Preferred Apo-2L receptor agonists include Apo-2L
 CC (especially amino acids 114-281 of the present sequence) and anti-DR4 or
 CC anti-DR5 receptor antibodies. Exposure of the cancer cells to CPT-11 and
 CC Apo-2L receptor agonist leads to upregulation of DR4 and DR5 receptors,
 CC directing the cells towards an apoptotic pathway rather than cell cycle
 CC arrest and possible DNA repair, thus providing enhanced antitumour
 CC activity. An example illustrates the synergistic inhibition of tumour
 CC growth by Apo-2L and CPT-11 in athymic nude mice injected s.c. with human
 CC COLO205 colon carcinoma cells
 XX
 XX Sequence 281 AA;
 Query Match 100.0%; Score 1287; DB 5; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYKSGIACFLKEDDSYNDPDEENSMNSPCQVQKQLRQVVKMLRTSEE 60
 DB 39 TNELKQMDKYKSGIACFLKEDDSYNDPDEENSMNSPCQVQKQLRQVVKMLRTSEE 98

QY 61 TISTVQKQKQNISPLVREGRQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
 |||||
 Db 99 TISTVQKQKQNISPLVREGRQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
 |||||
 QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDP 180
 |||||
 Db 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDP 218
 |||||
 QY 181 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 |||||
 Db 219 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 |||||
 QY 241 LVG 243
 |||||
 Db 279 LVG 281
 |||||

RESULT 23
 ABP51954
 ID ABP51954 standard; protein; 281 AA.
 AC ABP51954;
 XX
 DT 09-OCT-2002 (first entry)
 XX
 DE Human Apo-2 ligand protein sequence SEQ ID NO:4.
 XX
 KW Bacterial host; protease; degP; prc; spr; anti-VEGF antibody; antibody;
 KW humanised; Apo2 ligand; anti-CD18; anti-tissue factor; 2C4; anti-CD20;
 KW anti-vascular endothelial growth factor; anti-Her-2; anti-CD40; Fab;
 KW anti-CD11a; Fab'; Fab'2; Fab'2-leucine zipper fusion; anti-VEGF Fab.
 XX
 OS Homo sapiens.
 XX
 FN WO200248376-A2.
 XX
 PD 20-JUN-2002.
 XX
 PF 07-DEC-2001; 2001WO-US047581.
 XX
 PR 14-DEC-2000; 2000US-0256162P.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX
 FI Chen CY;
 XX
 DR WPI; 2002-583522/62.
 XX
 DR N-PSDB; ABQ73920.
 XX
 PT Novel Escherichia coli strain useful for producing polypeptide, deficient
 PT in degP and prc encoding protease, and harboring mutant spr gene, product
 PT of gene suppresses growth phenotypes of strains harboring prc mutants.
 XX
 PS Example 1; Fig 4; 63pp; English.

CC The present invention describes an Escherichia coli strain (I) deficient
 CC in chromosomal degP and prc encoding protease DegP and Prc, respectively,
 CC and harbouring a mutant spr gene, the product of mutant spr gene
 CC suppresses growth phenotypes exhibited by strains harbouring prc mutants.
 CC (I) is useful for producing a polypeptide, by culturing (I) comprising
 CC nucleic acid encoding the polypeptide, which is heterologous to the
 CC strain, such that the nucleic acid is expressed, and recovering the
 CC heterologous polypeptide from the strain. The heterologous polypeptide is
 CC proteolytically sensitive. Culturing of (I) is performed in a fermentor
 CC under conditions of high- or low-cell density fermentation. The
 CC polypeptide is recovered from the periplasm or culture medium of the
 CC strain. The polypeptide is an antibody (humanised or full-length
 CC antibody) or Apo2 ligand. The antibody is an anti-CD18, anti-vascular
 CC endothelial growth factor (VEGF), anti-tissue factor, 2C4, anti-Her-2,
 CC anti-CD20, anti-CD40, or anti-CD11a antibody. The antibody is also an
 CC antibody fragment having a light chain (kappa light chain). The antibody
 CC fragment is a Fab, Fab', Fab'2 or Fab'2-leucine zipper fusion, anti-CD18
 CC Fab'2-leucine zipper fusion, anti-tissue factor Fab'2-leucine zipper

CC fusion or anti-VEGF Fab, with or without a histidine or lysine tag, anti-
 CC tissue factor Fab'2-leucine zipper fusion with a 6-histidine tag, or anti-
 CC -CD18 Fab'2-leucine zipper fusion with a 6-histidine tag, and anti-CD18
 CC Fab'2-leucine zipper fusion with a 6-lysine tag. The present sequence
 CC represents a human Apo-2 ligand amino acid sequence from the present
 CC invention
 XX
 SQ Sequence 281 AA;
 Query Match 100.0%; Score 1287; DB 5; Length 281;
 Best Local Similarity 100.0%; Pred. No. 2.3e-117;
 Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TNELKQMDKYKSGIACFLKEDDSYDNDDESMNSPCQVQKWLQRLVKMLRTSEE 60
 |||||
 Db 39 TNELKQMDKYKSGIACFLKEDDSYDNDDESMNSPCQVQKWLQRLVKMLRTSEE 98
 |||||
 QY 61 TISTVQKQKQNISPLVREGRQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
 |||||
 Db 99 TISTVQKQKQNISPLVREGRQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
 |||||
 QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDP 180
 |||||
 Db 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQIYKYTSYDP 218
 |||||
 QY 181 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
 |||||
 Db 219 PILLMKSARNCSWCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
 |||||
 QY 241 LVG 243
 |||||
 Db 279 LVG 281
 |||||

RESULT 24
 AAO19095
 ID AAO19095 standard; protein; 281 AA.
 XX
 AC AAO19095;
 XX
 DT 22-NOV-2002 (first entry)
 XX
 DE C neoformans antigen expressing dendritic cell related protein #4.
 XX
 KW Human; fungicide; fungal infection; dendritic cell; antigen;
 KW Cryptococcus neoformans; vaccine; immunostimulant.
 XX
 OS Homo sapiens.
 XX
 FN WO200266053-A2.
 XX
 PD 29-AUG-2002.
 XX
 PF 14-DEC-2001; 2001WO-US048288.
 XX
 PR 04-JAN-2001; 2001US-0259653P.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 FI Thomas EK;
 XX
 DR WPI; 2002-674896/72.
 XX
 PT Producing a population of activated, Cryptococcus neoformans antigen-
 PT presenting dendritic cells for preventing or treating C. neoformans
 PT infection comprises causing the obtained dendritic cells to present the
 PT antigen.
 XX
 PS Disclosure; Page 29-30; 32pp; English.
 CC
 CC The present invention relates to a method of producing a population of
 CC activated, Cryptococcus neoformans antigen-presenting dendritic cells,
 CC comprising causing the obtained dendritic cells to present the antigen

CC and maturing the dendritic cells. The activated, C. neoformans antigen-
CC expressing dendritic cells are useful for treating, or as vaccines or
CC vaccine adjuvants against, C. neoformans infection, or for generating
CC antigen-specific T cells. The present sequence is a human protein shown
CC in the exemplification of the invention
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGIACFLKEDDSYWDPNDESMSPCWQVKQLRQVLRKMLRTSEE 60
DB 39 TNELKQMDKYSGIACFLKEDDSYWDPNDESMSPCWQVKQLRQVLRKMLRTSEE 98
QY 61 TISTVQEKQNIPLVREGRQVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQNIPLVREGRQVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPD 180
DB 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPD 218
QY 181 PILLKMSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLKMSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 25
AAU79593
ID AAU79593 standard; protein; 281 AA.
XX
AC AAU79593;
XX
DT 24-SEP-2002 (first entry)
XX

DE Human TNF-related apoptosis inducing ligand (TRAIL) protein.
XX
KW Human; cytostatic; neuroprotective; immunosuppressive; splice variant;
KW tumour necrosis factor; TNF; TNF-related apoptosis inducing ligand;
KW TRAIL; apoptosis; programmed cell death; differentiation; development;
KW cytokine; Apo-2 ligand; Apo-2L; nuclear factor-B; NF-B;
KW type I interferon; tumour; antitumour; gene therapy; cytotoxic; cancer;
KW therapeutic; neurodegenerative disease; autoimmune disease; aging;
KW chromosome 3q26.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT Domain 1..16
FT Domain /note= "Cytoplasmic domain"
FT Domain 17..38
FT Domain /note= "Transmembrane domain"
FT Domain 39..281
FT Domain /note= "Extracellular domain"
FT Domain 118..256
FT Domain /note= "TNF domain"

XX US2002061525-A1.
XX
XX 23-MAY-2002.
XX
XX 16-MAY-2001; 2001US-00855544.
XX
XX 16-MAY-2000; 2000IL-00136156.
XX
XX (YELI/) YELIN R.
XX (KHOS/) KHOSRAVI R.

PA (SAVI/) SAVITZKY K.
XX
XX Yelin R, Khosravi R, Savitzky K;
XX WPI; 2002-479259/51.
DR
XX
XX
PT New splice variants of tumor necrosis factor-related apoptosis inducing
PT ligand (TRAIL) isolated from B-lymphocytes and liver, useful to treat
PT diseases or disorders associated with low expression of the variants.
XX
XX
PS Disclosure; Fig 9; 29pp; English.

CC The invention discloses isolated, naturally occurring, polypeptide splice
CC variants of human tumour necrosis factor (TNF)-related apoptosis inducing
CC ligand (TRAIL). Apoptosis, or programmed cell death, occurs during normal
CC cellular differentiation and development of multicellular organisms.
CC Apoptosis is induced by certain cytokines which include TNF and TRAIL
CC (also referred to as Apo-2 ligand, Apo-2L). TRAIL is a type II membrane
CC protein which induces apoptosis and nuclear factor-B (NF-B) activation in
CC many tissues and cells. Receptors for TRAIL include two death domain
CC containing receptors, DR4 and DR5, as well as two decoy receptors, DCR1
CC and DCR2, lacking the intracellular signalling death domain. TRAIL,
CC induced by type I interferons, induces apoptosis in tumour cells, whereas
CC normal cells are relatively resistant without showing significant toxic
CC side effects. Thus, TRAIL has the potential to be a very useful
CC antitumour agent. The naturally occurring splice variants may differ in
CC their cellular distribution, expression levels/timing and activity.
CC Determining these factors could provide possible mechanisms for the
CC induction of apoptosis of tumours cells. The splice variant polypeptides
CC and polynucleotides can be used in gene therapy, to raise antibodies, to
CC detect the levels, distribution and ratios of expression of TRAIL, and
CC its splice variants, in a biological sample and to identify compounds
CC which bind the variant TRAIL products and modulate its activity (agonists
CC and antagonists). Pharmaceutical compositions, comprising an expression
CC vector or any of the amino acid sequences, are useful for causing a
CC cytotoxic effect in cancer cells and for treatment of diseases which can
CC be ameliorated, cured or prevented by lowering or raising the level of
CC the amino acid sequences. The antibodies may also have a therapeutic
CC utility in blocking or decreasing the activity of the TRAIL variant
CC products. Diseases that may be treated include cancer, neurodegenerative
CC diseases, autoimmune diseases, diseases involved in the non-normal
CC development of tissues and aging. TRAIL's gene is located on chromosome
CC 3q26. The sequence presented is the wild-type human TNF-related apoptosis
CC inducing ligand (TRAIL) protein

SQ Sequence 281 AA;
Query Match 100.0%; Score 1287; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGIACFLKEDDSYWDPNDESMSPCWQVKQLRQVLRKMLRTSEE 60
DB 39 TNELKQMDKYSGIACFLKEDDSYWDPNDESMSPCWQVKQLRQVLRKMLRTSEE 98
QY 61 TISTVQEKQNIPLVREGRQVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQNIPLVREGRQVAAHITGTRGNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPD 180
DB 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQYIYKTSYPD 218
QY 181 PILLKMSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLKMSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 26

CC the Apo-2 ligand protein was measured on human lymphoid cells

XX Sequence 281 AA;

QY Query Match 100.0%; Score 1287; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELQMODKYSKSGIACFLKEDDSYNDPNDDESNPCWQVKWQLQOLVYKMLRTSEE 60
DB 39 TNELQMODKYSKSGIACFLKEDDSYNDPNDDESNPCWQVKWQLQOLVYKMLRTSEE 98
QY 61 TISTVQEKQONISPLVVRERGQORVAHAHITGRGRSNTLSSPNSKNEKALGRKINSWSSSR 120
DB 99 TISTVQEKQONISPLVVRERGQORVAHAHITGRGRSNTLSSPNSKNEKALGRKINSWSSSR 158
QY 121 SGHSFLSNLHLRNGELVHKGFFYIYSQTYFRQBEIKENTKNDKQWQVYIYKYTSYVD 180
DB 159 SGHSFLSNLHLRNGELVHKGFFYIYSQTYFRQBEIKENTKNDKQWQVYIYKYTSYVD 218
QY 181 PILLMKSRNSCWSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSRNSCWSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LNG 243
DB 279 LNG 281

RESULT 27
ABU10205
ID ABU10205 standard; protein; 281 AA.
AC ABU10205;
XX 11-AUG-2003 (first entry)
DT Human Apo-2 ligand.
DE Human; Apo-2 ligand; apoptosis; gene therapy; inflammation; cancer;
KW neurodegenerative disease; immunosuppressive; tissue typing.
XX Homo sapiens.
OS
XX US2003004313-A1.
PN 02-JAN-2003.
XX 28-MAR-2002; 2002US-00112193.
XX 23-SEP-1996; 96US-0026943P.
PR 11-SEP-1997; 97US-00928065.
XX (GETH) GENENTECH INC.
PI Ashkenazi AJ;
XX WPI; 2003-438872/41.
DR N-PSDB; ACA61696.
XX New isolated Apo-3 polypeptides, useful for stimulating or inducing
PT apoptotic activity in mammalian cells, e.g. cancer cells, or for in vivo
or ex vivo gene therapy techniques.
XX Example 4; Fig 4; 50pp; English.
XX The invention relates to an isolated Apo-3 polypeptide. The Apo-3
CC polypeptides are useful for stimulating or inducing apoptotic activity in
CC mammalian cells e.g. cancer cells, or for in vivo or ex vivo gene therapy
CC techniques. The Apo-3 chimeric molecules are useful for inhibiting
CC apoptosis, or as immunogens used in generating antibodies. The
CC antagonistic antibodies may be used to block excessive apoptosis, for
CC instance in neurodegenerative disease, or to block potential autoimmune/
CC

ABG73861 standard; protein; 281 AA.
XX ABG73861;
XX 03-APR-2003 (first entry)
XX Human Apo-2 ligand protein.
XX Human; Apo-2; apoptosis; induce apoptosis; inhibit apoptosis; TNFR;
KW nuclear factor-kappa B; NF-kappa B; Apo-2 ligand; AIDS;
KW tumour necrosis factor receptor; acquired immunodeficiency syndrome;
KW Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis;
KW multiple sclerosis; retinitis pigmentosa; cerebellar degeneration;
KW aplastic anaemia; myocardial infarction; stroke; reperfusion injury;
KW toxin-induced liver disease; cancer; lupus; herpes virus infection.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FT Domain 15..40
FT /note= "Transmembrane domain"
FT Domain 41..281
FT /note= "Extracellular domain"
FT Modified-site 109
FT /note= "N-glycosylated"
XX US6462176-B1.
XX 08-OCT-2002.
XX 11-SEP-1997; 97US-00928069.
XX 23-SEP-1996; 96US-0026943P.
XX (GETH) GENENTECH INC.
XX Ashkenazi AJ;
XX WPI; 2003-173840/17.
DR N-PSDB; ABX15469.
XX Novel isolated Apo-3 polypeptide useful for inducing apoptosis in
PT mammalian cells, for generating antibodies, in affinity purification
PT techniques, and in competitive-type receptor binding assays.
XX Example 4; Fig 4; 52pp; English.
XX The invention relates to an Apo-3 polypeptide having an extracellular
CC domain (ECD) sequence and a death domain sequence. The Apo-3 polypeptide
CC has been found to stimulate or induce apoptotic activity in mammalian
CC cells. Human Apo-3 exhibits similarities to the tumour necrosis factor
CC receptor (TNFR) family of polypeptides. The invention also relates to a
CC chimeric molecule comprising an extracellular domain sequence comprising
CC residues 1-198 of Apo-3 fused to a heterologous amino acid sequence. The
CC Apo-3 polypeptide is useful therapeutically to induce apoptosis in
CC mammalian cells. Decreased levels of apoptosis has been associated with
CC conditions such as cancer, lupus, and herpes virus infection. Increased
CC levels of apoptosis are associated with diseases such as acquired
CC immunodeficiency syndrome (AIDS), Alzheimer's disease, Parkinson's
CC disease, amyotrophic lateral sclerosis, multiple sclerosis, retinitis
CC pigmentosa, cerebellar degeneration, aplastic anaemia, myocardial
CC infarction, stroke, reperfusion injury, and toxin-induced liver disease.
CC The Apo-3 polypeptide is also useful in non-therapeutic applications such
CC as in quantitative diagnostic assays as a control against which samples
CC containing unknown quantities of Apo-3 may be prepared, in generating
CC antibodies, as standards in assays for Apo-3, in affinity purification
CC techniques, and in competitive-type receptor binding assays. The chimeric
CC molecule is useful therapeutically to inhibit apoptosis or nuclear factor
CC -kappa B (NF-kappa B) induction, or as an immunogen for producing anti-
CC Apo-3 antibodies. The present sequence represents polypeptide sequence of
CC the human Apo-2 ligand protein which is also reported to be involved in
CC apoptotic cell death. In the current invention the apoptotic activity of

CC inflammatory effects of Apo-3 resulting from NF-kappaB activation. The
CC nucleic acid sequences are useful as diagnostics for tissue-specific
CC typing, for preparing Apo-3 polypeptides, or for generating transgenic or
CC knockout animals. The transgenic or knockout animals are useful in
CC developing and screening of therapeutically useful reagents. The present
CC sequence represents the amino acid sequence of human Apo-2 ligand
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 1287; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMDKYSKSGTACFLKDDSYWDPNDESNPCWQVQWLRQVLRKMLRTSEE 60
DB 39 TNELKQMDKYSKSGTACFLKDDSYWDPNDESNPCWQVQWLRQVLRKMLRTSEE 98
QY 61 TISTVQEKQNISPLVRERGPQVAAHITGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQNISPLVRERGPQVAAHITGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVIEHKEFYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYPD 180
DB 159 SGHSFLSNLHRLNGELVIEHKEFYIYSQTYFRFOEIKENTKNDKQVQYIKYTSYPD 218
QY 181 PILLMKSARNSCWSKDAEYGLYSIYQGIFELKENDRIFFSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNSCWSKDAEYGLYSIYQGIFELKENDRIFFSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281
RESULT 28
ID ABU71443 standard; protein; 281 AA.
XX ABU71443;
AC ABU71443;
DT 09-JUN-2003 (first entry)
DE Human neoplasia inhibiting PRO polypeptide PRO1096.
XX Human; tumour; cancer; neoplasia; liver cancer; sarcoma; breast cancer;
KW ovarian cancer; renal cancer; colorectal cancer; melanoma;
KW uterine cancer; prostate cancer; lung cancer; bladder cancer; leukaemia;
KW gastric cancer; pancreatic cancer; vulval cancer; thyroid cancer;
KW central nervous system cancer; hepatic carcinoma; glioblastoma;
KW neuronal disorder; glial disorder; astrocytal disorder;
KW hypothalamic disorder; glandular disorder; macrophegal disorder;
KW epithelial disorder; stromal disorder; blastocoelec disorder;
KW inflammatory disorder; angiogenic disorder; immunologic disorder.
XX
OS Homo sapiens.
XX
XX US2002192209-A1.
XX
XX 19-DEC-2002.
XX
XX 30-NOV-2001; 2001US-00001054.
XX
XX 17-SEP-1997; 97US-0059114P.
XX 27-MAR-1998; 98US-0079689P.
XX 30-MAR-1998; 98US-0079320P.
XX 24-APR-1998; 98US-0082999P.
XX 29-APR-1998; 98US-0083545P.
XX 12-MAY-1998; 98US-0085149P.
XX 02-JUN-1998; 98US-0087607P.
XX 11-JUN-1998; 98US-0088858P.
XX 25-JUN-1998; 98US-0090691P.
XX 17-AUG-1998; 98US-0096891P.
XX 17-AUG-1998; 98US-0096894P.

PR 10-SEP-1998; 98US-0099803P.
PR 10-SEP-1998; 98WO-US018824.
PR 14-SEP-1998; 98US-0100263P.
PR 15-SEP-1998; 98US-0100390P.
PR 23-SEP-1998; 98US-0101476P.
PR 10-NOV-1998; 98US-0107783P.
PR 18-NOV-1998; 98US-0108849P.
PR 19-NOV-1998; 98US-00180997.
PR 15-DEC-1998; 98US-0112420P.
PR 22-DEC-1998; 98US-00218517.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99WO-US0000106.
PR 12-JAN-1999; 99US-0115554P.
PR 12-JAN-1999; 99US-0115558P.
PR 20-JAN-1999; 99US-0116333P.
PR 08-MAR-1999; 99WO-US0005028.
PR 10-MAR-1999; 99US-0123618P.
PR 12-APR-1999; 99US-00284291.
PR 20-APR-1999; 99WO-US0008615.
PR 27-APR-1999; 99US-0131294P.
PR 02-JUN-1999; 99WO-US012252.
PR 22-JUN-1999; 99US-0140650P.
PR 23-JUN-1999; 99US-0141037P.
PR 20-JUL-1999; 99US-0144758P.
PR 25-AUG-1999; 99US-00380137.
PR 01-SEP-1999; 99US-00380138.
PR 08-SEP-1999; 99WO-US020594.
PR 09-SEP-1999; 99US-00380913.
PR 18-OCT-1999; 99US-00403297.
PR 29-OCT-1999; 99US-0162506P.
PR 10-NOV-1999; 99US-00423741.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028634.
PR 02-DEC-1999; 99WO-US028551.
PR 09-DEC-1999; 99US-0170262P.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030999.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 18-FEB-2000; 2000WO-US004342.
PR 02-MAR-2000; 2000WO-US005841.
PR 03-MAR-2000; 2000US-0187202P.
PR 15-MAR-2000; 2000WO-US006884.
PR 30-MAR-2000; 2000WO-US008439.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 08-NOV-2000; 2000US-00709238.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 25-MAY-2001; 2001US-00866034.
PR 01-JUN-2001; 2001US-00872034.
PR 01-JUN-2001; 2001US-00872035.
PR 01-JUN-2001; 2001WO-US017800.
PR 14-JUN-2001; 2001US-00882636.
PR 20-JUN-2001; 2001WO-US019892.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 30-JUL-2001; 2001US-00918585.
PR 06-AUG-2001; 2001US-00924419.
PR 13-AUG-2001; 2001US-00927796.
PR 09-AUG-2001; 2001US-00929404.
PR 28-AUG-2001; 2001US-00941392.
PR 29-AUG-2001; 2001WO-US027059.

PR 04-SEP-2001; 2001US-00946374.
XX (GETH) GENENTECH INC.
PA Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W, Kabakoff RC;
XX Shelton DU, Smith V, Watanabe CK, Wood WI;
PI WPI; 2003-328851/06.
XX N-PSDB; ACAS8016.
XX Novel isolated PRO polypeptides e.g. PRO240, PRO381, PRO540, useful for
PT treating tumor, preferably cancer, or for treating neuronal, glial,
PT hypothalamic, stromal, inflammatory, angiogenic and immunologic
PT disorders.
XX Claim 32; Fig 54; 186pp; English.
XX The invention relates to an isolated secreted and transmembrane
CC polypeptide, designated as PRO polypeptide, PRO polypeptide lacking its
CC associated signal peptide or PRO polypeptide extracellular domain with or
CC without its associated signal peptide. The PRO polypeptide or an antibody
CC binding to it is useful for inhibiting the growth of a tumor cell. A
CC composition containing a PRO polypeptide is useful for inhibiting
CC neoplastic cell growth or for treating a tumour, preferably cancer (such
CC as liver, breast, ovarian, renal, colorectal, uterine, prostate, lung,
CC bladder, gastric, pancreatic, vulval, thyroid, central nervous system
CC cancer, hepatic carcinomas, sarcomas, glioblastomas, melanoma or
CC leukaemia) in a mammal. The PRO polypeptide is useful for identifying its
CC agonists. The PRO polypeptide or an antibody binding to it is useful in
CC the preparation of a medicament for treating a condition which is
CC responsive to the PRO polypeptide or an antibody binding to it. The PRO
CC polypeptide or an antibody binding to it is also useful for treating
CC neuronal glial, astrocytal, hypothalamic, glandular, macrophagal,
CC epithelial, stromal, blastocoealic, inflammatory, angiogenic and
CC immunologic disorders. The present sequence represents the amino acid
CC sequence of a PRO polypeptide of the invention
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117; Indels 0; Gaps 0;
Matches 243; Conservative 0; Mismatches 0;
QY 1 TNELQMDQKYSKSGIACFLKEDDSYDNDDEESMNSPCQVQWQLRQLVVKMLRTSEE 60
DB 39 TNELQMDQKYSKSGIACFLKEDDSYDNDDEESMNSPCQVQWQLRQLVVKMLRTSEE 98
QY 51 TISTVQEKQONISPLVREGRGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVREGRGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRQEEIKENTKDKQKQVQIYKTSYD 180
DB 159 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRQEEIKENTKDKQKQVQIYKTSYD 218
QY 181 PILLMKSARNSCWSDAEYGLYSYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAF 240
DB 241 LVG 243
279 LVG 281

RESULT 29
ABG72738
ID ABG72738 standard; protein; 281 AA.
XX AC ABG72738;
XX DT 17-FEB-2003 (first entry)
XX DE Human TNF-related apoptosis inducing ligand (TRAIL) protein.

XX Human; allergic disease; allergy; TNF; TRAIL; diagnosis;
KW tumour necrosis factor-related apoptosis inducing ligand;
KW atopic skin inflammation.
XX Homo sapiens.
XX WO200283946-A1.
XX 24-OCT-2002.
XX 01-MAR-2002; 2002WO-JP001914.
XX 06-APR-2001; 2001JP-00108631.
XX (GENO-) GENOX RES INC.
XX (NICE-) JAPAN GEN AGENCY NATION.
XX Sugita Y, Heishi M, Kagaya S, Gunji S, Tsujimoto G;
XX WPI; 2003-093037/08.
XX N-PSDB; ABX13715.
XX Measurement of the expression level of TNF related apoptosis inducing
PT ligand gene for diagnosis and examination of allergic disease and
PT screening agents for allergic disease treatment.
XX Disclosure; Page 51-52; 58pp; Japanese.
XX The invention discloses a method for examining allergic diseases, which
CC comprises measuring the expression level of tumour necrosis factor (TNF)-
CC related apoptosis inducing ligand (TRAIL) gene in a specimen from the
CC patient and comparing this level with the level in healthy persons. TRAIL
CC gene expression is decreased in patients. The nucleic acids and
CC polypeptide can be used to screen for agents for the treatment of
CC allergic diseases, possibly using a transgenic rodent as a model animal
CC for the disease, with effectiveness determined by changes in expression
CC levels or protein activity. The method is useful for the diagnosis,
CC examination, prevention and treatment of allergic diseases, including
CC atopic skin inflammation. The sequence presented is the human TRAIL
CC protein
XX
SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117; Indels 0; Gaps 0;
Matches 243; Conservative 0; Mismatches 0;
QY 1 TNELQMDQKYSKSGIACFLKEDDSYDNDDEESMNSPCQVQWQLRQLVVKMLRTSEE 60
DB 39 TNELQMDQKYSKSGIACFLKEDDSYDNDDEESMNSPCQVQWQLRQLVVKMLRTSEE 98
QY 61 TISTVQEKQONISPLVREGRGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVREGRGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRQEEIKENTKDKQKQVQIYKTSYD 180
DB 159 SGHSFLSNLHRLNGELVHEKGFYIYSQTYFRQEEIKENTKDKQKQVQIYKTSYD 218
QY 181 PILLMKSARNSCWSDAEYGLYSYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNSCWSDAEYGLYSYQGGIFELKENDRIFSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
279 LVG 281

RESULT 30
AAO29543
ID AAO29543 standard; protein; 281 AA.
XX

PS Claim 1; Col 45-48; 40pp; English.

XX The invention relates to an antibody that specifically binds: (a) the

CC human tumor necrosis factor (TNF) related apoptosis inducing ligand

CC (TRAIL) protein appearing as AB08558; (b) a soluble human TRAIL

CC polypeptide; (c) a polypeptide comprising amino acids 124-276 of

CC AB08558, or (d) a fragment of the TRAIL protein. Also included is an

CC antigen-binding fragment of the antibody (a monoclonal antibody), a

CC hybridoma cell line that produces the antibody. The antibody is used in

CC assays to detect the presence of TRAIL polypeptides, either in vitro or

CC in vivo, purifying TRAIL by affinity chromatography, blocking binding of

CC TRAIL to target cells and thus inhibiting a biological activity of TRAIL.

CC The antibody is useful for treating disorders mediated or exacerbated by

CC TRAIL, e.g. thrombotic microangiopathies, e.g. thrombotic

CC thrombocytopenic purpura (TTP), adult haemolytic uraemic syndrome (HUS)

CC (even though it can strike children as well) small blood vessel clotting

CC disorders e.g., cardiac problems in paediatric AIDS patients and systemic

CC lupus erythematosus (SLE). The present sequence represents human TRAIL

XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 6; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.3e-117;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDESNMSPCWQVKQLRQLVRKMLRTSEE 60

Db 39 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDESNMSPCWQVKQLRQLVRKMLRTSEE 98

Qy 61 TISTVQEKQNIPLVREGRQORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 120

Db 99 TISTVQEKQNIPLVREGRQORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 158

Qy 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQKVQIYKYTSYPD 180

Db 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQKVQIYKYTSYPD 218

Qy 181 PILLMKSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240

Db 219 PILLMKSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

Qy 241 LVG 243

Db 279 LVG 281

RESULT 32

ABR42313

ID ABR42313 standard; protein; 281 AA.

XX

AC ABR42313;

DT 11-AUG-2003 (first entry)

XX

DE Human TRAIL protein.

XX

KW Human; TRAIL; tumour necrosis factor; ligand; cytostatic;

KW immunomodulator; osteopathic.

XX

OS Homo sapiens.

XX

PN WO2003040307-A2.

XX

PD 15-MAY-2003.

XX

PF 25-JUL-2002; 2002WO-US023782.

XX

PR 27-JUL-2001; 2001US-0307838P.

XX

PA (HUMA-) HUMAN GENOME SCI INC.

XX

PI Hilbert DE, Rosen CA;

XX

DR WPI: 2003-430659/40.

DR N-PSDB; ACC57899.

XX

PT New heteromultimeric complex having a first polypeptide member of the

CC tumor necrosis factor (TNF) ligand family, and a second different member

CC of TNF ligand family, useful for treating cancer, osteoporosis or an

PT autoimmune disease.

XX

PS Disclosure; Page 364-365; 388pp; English.

XX

CC The present sequence is the protein sequence of human TRAIL polypeptide.

CC The invention relates to compositions comprising heterotrimeric complexes

CC of tumour necrosis factor (TNF) ligand family members, and their use in

CC the detection, prevention and treatment of disease. In one embodiment,

CC the heterotrimeric complex comprises full-length or extracellular

CC portions of TRAIL and full-length or extracellular portions of other TNF

CC ligand family members, preferably RANKL. The heterotrimeric complexes of

CC the invention are useful for treating an autoimmune disease, cancer or

CC osteoporosis, and particularly for inhibiting cancer cell proliferation,

CC increasing B cell proliferation, or inducing apoptosis of T cells. A

CC claimed method of inducing apoptosis of T cells comprises administering a

CC heterotrimeric complex consisting of FasL and LIGHT, TNF-alpha,

CC lymphotixin-beta or TRAIL. A claimed method of inhibiting cancer cell

CC proliferation involves administering a heterotrimeric complex consisting

CC of TRAIL and CD40L or RANK. A claimed method of treating osteoporosis

CC comprises administering an antibody against a complex comprising RANKL

CC and TRAIL

XX

SQ Sequence 281 AA;

Query Match 100.0%; Score 1287; DB 6; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.3e-117;

Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDESNMSPCWQVKQLRQLVRKMLRTSEE 60

Db 39 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDESNMSPCWQVKQLRQLVRKMLRTSEE 98

Qy 61 TISTVQEKQNIPLVREGRQORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 120

Db 99 TISTVQEKQNIPLVREGRQORVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 158

Qy 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQKVQIYKYTSYPD 180

Db 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQKVQIYKYTSYPD 218

Qy 181 PILLMKSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240

Db 219 PILLMKSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

Qy 241 LVG 243

Db 279 LVG 281

RESULT 33

ABG71905

ID ABG71905 standard; protein; 281 AA.

XX

AC ABG71905;

XX

DT 20-JAN-2003 (first entry)

XX

DE Human TRAIL receptor-associated protein.

XX

KW Human; TRAIL receptor; tumour necrosis factor; TNF;

KW light chain variable region TNF-related apoptosis-inducing ligand;

KW antibody; VH; VL; cancer; heavy chain variable region; TR4; TR5; TR7;

KW TR10; apoptosis; hyperproliferative disorder; hybridoma cell line;

KW Kaposi's sarcoma; graft-versus-host disease; GVHD; infectious disease;

KW AIDS; acquired immunodeficiency syndrome; neurodegenerative disorder;

KW Alzheimer's disease; Parkinson's disease; autoimmune disorder;

KW multiple sclerosis; Behcet's disease; lupus erythematosus;

KW	inflammatory disease; rheumatoid arthritis; psoriasis; wound healing;	Db	39	TNELKQMDKYSGIACFLKEDDSYWDPNDBESMNSPCWQVQWLQRLVRKMLTSEE	98
KW	cardiovascular disorder; angiogenesis; immune response;	Qy	61	TISTVOEKQONISPLVRERGPORVAHIITGTGRSNTLSSPNSKNEKALGRKINSWESSR	120
XX	chemotherapeutic agent.	Db	99	TISTVOEKQONISPLVRERGPORVAHIITGTGRSNTLSSPNSKNEKALGRKINSWESSR	158
OS	Homo sapiens.	Qy	121	SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDP	180
PN	WO200279377-A2.	Db	159	SGHSFSLNHLRNGELVIHEKGFYIYSQTYFRFQEEIKENTKNDKQMVQYIYKYTSYDP	218
PD	10-OCT-2002.	Qy	181	PILLMSARNSCWSKDAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF	240
XX	07-NOV-2001; 2001WO-US042996.	Db	219	PILLMSARNSCWSKDAEYGLYSIYGGIFELKENDRIFVSVTNEHLIDMDHEASFGAF	278
XX	08-NOV-2000; 2000US-0246612P.	Qy	241	LVG 243	
PR	16-NOV-2000; 2000US-0248847P.	Db	279	LVG 281	
PR	27-NOV-2000; 2000US-0252904P.				
PR	04-JUN-2001; 2001US-0295018P.				
PR	09-OCT-2001; 2001US-0327359P.				
XX	(HUMA-) HUMAN GENOME SCI INC.				
PA	Salcedo T, Roschke V, Ruben SM, Rosen CA;				
PI	WPI; 2003-040669/03.				
DR	Novel antibody for treating, or preventing disease or disorder, comprises				
PT	amino acid sequence having identity to other amino acid sequence of				
PT	either variable heavy/light chain-complementarity determining regions.				
XX	Disclosure; Page 366; 375pp; English.				
PS	The invention relates to an isolated antibody comprising a first amino				
XX	acid sequence having 95 % identity to a second amino acid sequence of				
CC	either variable heavy chain or light chain-complementarity determining				
CC	regions (VHCDRI1/VLCDRI1, VHCDRI2/VLCDRI2 or VHCDRI3/VLCDRI3 appearing as				
CC	ABG71906-ABG71911 being specific for human TRAIL receptors 1-4 (TNF				
CC	(tumour necrosis factor)-related apoptosis-inducing ligand receptor, also				
CC	known as TR4, TR5, TR7 and TR10). Also included are an isolated cell that				
CC	produces the antibody, an antibody that binds the same epitope on a TR4				
CC	polypeptide as the antibodies detailed above, detecting expression of a				
CC	TR4 polypeptide (or detecting, diagnosing, prognosing or monitoring				
CC	cancers, and other hyperproliferative disorders) using the antibodies, a				
CC	hybridoma cell line selected from the hybridoma cell lines contained in				
CC	ATCC Deposit No. PTA-3149, PTA-2687, PTA-3369, PTA-2730, PTA-2729, PTA-				
CC	2728, PTA-3368, and PTA-2731 and the antibodies expressed by these				
CC	hybridoma cell lines. The antibodies of the invention are useful for				
CC	diagnosing or treating a disease or disorder associated with increased or				
CC	decreased apoptosis, e.g. cancer (such as colon, breast, uterine,				
CC	pancreatic, lung, gastrointestinal, and Kaposi's sarcoma), graft-versus-				
CC	host disease (GVHD), infectious disease, acquired immunodeficiency				
CC	syndrome (AIDS), or neurodegenerative disorders (e.g. Alzheimer's				
CC	disease, Parkinson's disease), autoimmune disorders like multiple				
CC	sclerosis, Behcet's disease, lupus erythematosus, inflammatory diseases				
CC	such as rheumatoid arthritis, and psoriasis, cardiovascular disorders, in				
CC	promoting angiogenesis, wound healing, and in regulating immune response.				
CC	Many other diseases and disorders are listed in the specification. The				
CC	antibody is administered in combination with a chemotherapeutic agent				
CC	selected from irinotecan, paclitaxel (TAXOL (RTM), and gemcitabine. The				
CC	antibody is useful as a diagnostic tool to monitor the expression of				
CC	TRAIL receptor expression on cells, to detect, purify, and target the				
CC	polypeptides, and in immunoassays for qualitatively and quantitatively				
CC	measuring levels of TRAIL receptor polypeptides. The present sequence is				
CC	a human TRAIL receptor associated protein. Note: The present sequence is				
CC	included in the sequence listing but is not referred to anywhere else in				
CC	the specification				
XX	Sequence 281 AA;				
Qy	Query Match 100.0%; Score 1287; DB 6; Length 281;				
XX	Best Local Similarity 100.0%; Pred. No. 2.3e-117;				
XX	Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	1 TNELKQMDKYSGIACFLKEDDSYWDPNDBESMNSPCWQVQWLQRLVRKMLTSEE 60				

Db 219 PILLMKARNSCWSDAEYGLYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
Db 279 LVG 281
RESULT 36
ID AAO31151 standard; protein; 281 AA.
XX AAO31151;
DT 06-OCT-2003 (first entry)
XX Human TNF-related apoptosis-inducing ligand (TRAIL).
XX Human; protein coordinate data; heavy chain variable domain; VH; cancer;
KW complementarity determining region; CDR; light chain variable domain; VL;
KW TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5;
KW DR5; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand;
KW Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma;
KW glioblastoma; graft versus host disease; antibody therapy; neoplastic;
KW AIDS; acquired immune deficiency syndrome; neurodegenerative disorder;
KW immunosuppressive; neuroprotective; antibody therapy; antibody.
XX Homo sapiens.
XX WO2003054216-A2.
XX 03-JUL-2003.
XX 19-DEC-2002; 2002WO-US040597.
XX 20-DEC-2001; 2001US-0341237P.
XX 05-APR-2002; 2002US-0369877P.
XX 04-JUN-2002; 2002US-0384828P.
XX 18-JUL-2002; 2002US-0396591P.
XX 15-AUG-2002; 2002US-0403370P.
XX 13-NOV-2002; 2002US-0425737P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;
XX WPI; 2003-569250/53.
XX New antibody or its fragment, useful for treating, preventing or
PT ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
PT gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host
PT disease, AIDS.
XX Disclosure; Page 297-298; 301pp; English.
XX The invention relates to an isolated antibody or its fragments such as
CC VHCDR1 (heavy chain variable domain complementarity determining region),
CC VHCDR2, VHCDR3, VLCDR1 (light chain variable domain complementarity
CC determining region), VLCDR2 or VLCDR3. The antibody or its fragment
CC immunospecifically binds TRAIL (tumour necrosis factor; TNF-related
CC apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as
CC TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The
CC antibody or its fragment is useful for treating, preventing or
CC ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
CC gastrointestinal cancer or Kaposi's sarcoma or cancer of the central
CC nervous system such as medulloblastoma, neuroblastoma or glioblastoma or
CC graft versus host disease, AIDS (acquired immune deficiency syndrome) or
CC a neurodegenerative disorder. The invention is useful in antibody
CC therapy. The present sequence is human TRAIL
XX Sequence 281 AA;
SQ Query Match 100.0%; Score 1287; DB 6; Length 281;

Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMDKYKSGIACFLKEDDSYDNDDESMNSPCWQVKWOLRQIVRKMLRTSEE 60
Db 39 TNELKQMDKYKSGIACFLKEDDSYDNDDESMNSPCWQVKWOLRQIVRKMLRTSEE 98
QY 61 TISTVQEKQKNISPLVREERGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQKNISPLVREERGQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLNLHRLNGELVIHEKGFYIYSQYFFQBEIKENTKDKQKVQYIYKTSYPD 180
Db 159 SGHSFLNLHRLNGELVIHEKGFYIYSQYFFQBEIKENTKDKQKVQYIYKTSYPD 218
QY 181 PILLMKARNSCWSDAEYGLYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLMKARNSCWSDAEYGLYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
Db 279 LVG 281
RESULT 37
ID ABO25125 standard; protein; 281 AA.
XX ABO25125;
XX 05-SEP-2003 (first entry)
XX Human TNF-related apoptosis inducing ligand TRAIL Incyte 059509CD1.
XX Human; DNA methylation; cancer; colon cancer.
XX Homo sapiens.
XX US2003013099-A1.
XX 16-JAN-2003.
XX 07-MAR-2002; 2002US-00093766.
XX 19-MAR-2001; 2001US-0277380P.
XX (LASE/) LASEK A K W.
XX (JONE/) JONES D A.
XX (KARP/) KARP A R.
XX Lasek AKW, Jones DA, Karpf AR;
XX WPI; 2003-503249/47.
XX N-PSDB; ACD42246.
XX New combination comprising cDNAs that are expressed in a disorder or
PT process associated with DNA methylation, useful for diagnosing, staging,
PT treating or monitoring treatment of cancer, e.g. colon cancer.
XX Disclosure; Page 56-57; 66pp; English.
XX The invention relates to a combination comprising cDNAs which are
CC expressed in a disorder or process associated with DNA methylation. The
CC combination and cDNAs are useful for diagnosing, staging, treating or
CC monitoring treatment of cancer, e.g. colon cancer and for detecting
CC changes in expression of genes encoding proteins that are associated with
CC DNA methylation. The protein is useful for screening molecules or
CC compounds to identify, at least one ligand that binds to the protein and
CC for producing an antibody. The present sequence represents the amino acid
CC sequence of a protein expressed in a disorder or process associated with
XX DNA methylation
XX Sequence 281 AA;
SQ

Query Match 100.0%; Score 1287; DB 6; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKGIACFLKEDDSYDNDDESMNSPCWQVQWQLRQLVRLMILTSEE 60
DB 39 TNELKQMDKYSGKGIACFLKEDDSYDNDDESMNSPCWQVQWQLRQLVRLMILTSEE 98

QY 61 TISTVQEKQNIPLVREGRGQVAAHITGTRGSNTLSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQNIPLVREGRGQVAAHITGTRGSNTLSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQYFRFQBEIKENTKDKQWQYIYKTSYDP 180
DB 159 SGHSFSLNHLRNGELVIHEKGFYIYSQYFRFQBEIKENTKDKQWQYIYKTSYDP 218

QY 181 PILLKSGARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLKSGARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
DB 279 LVG 281

RESULT 38
ADB61471
ID ADB61471 standard; protein; 281 AA.
XX
AC ADB61471;
XX
XX 04-DEC-2003 (first entry)
XX
DE Native human Apo-2 ligand protein.
XX
KW Apo-2 ligand; DR5 Apo2L complex; receptor contact region;
KW high solvent accessibility; cytostatic; antiarthritic; neuroprotective;
KW trimer; apoptosis; DR4 receptor; DR5 receptor; colon; colorectal cancer;
KW lung; breast; immune-related disease; arthritis; multiple sclerosis;
KW native; human.
XX
OS Homo sapiens.
XX
XX WO2003029420-A2.
XX
XX 10-APR-2003.
XX
XX 01-OCT-2002; 2002WO-US031210.
XX
XX 02-OCT-2001; 2001US-0326622P.
XX
XX (GETH) GENENTECH INC.
XX
XX Kelley RP, Lindstrom SH;
XX
XX WPI; 2003-541400/51.
XX
XX N-PSDB; ADB61470.
XX
XX Novel isolated Apo-2 ligand variant polypeptide useful for treating
XX cancer or an immune-related disease such as multiple sclerosis, comprises
XX amino acid substitutions in the native sequence of the Apo-2 ligand.
XX
XX Claim 1; Fig 1; 92pp; English.
XX
XX The invention relates to a novel isolated Apo-2 ligand variant
XX polypeptide having a sequence that differs from the native sequence
XX having 281 amino acids given in specification. The Apo-2 ligand variant
XX polypeptide is selected from a polypeptide having substitutions at
XX residue positions identified from x-ray crystal structure of the
XX DR5-Apo2L complex. The polypeptide having the substitutions made at
XX residue position(s) selected from 20 positions such as S96C, S101C,
XX S111C, V114C, R115C, E116C, N134C, N140C, E144C, N152C, S153C, R170C,

CC R170K, R170S, K179C, D234C, E249C, R255C, E264C, such that the
CC residue position is, outside of the receptor contact region of the
CC DR5-Apo2L complex, and displays high solvent accessibility in the crystal
CC structure of the DR5-Apo2L complex. The Apo-2 ligand variant polypeptide
CC and further compositions have the following activities: cytostatic,
CC antiarthritic and neuroprotective. The Apo-2 ligand variant polypeptide,
CC an Apo-2 ligand composition or an Apo-2 ligand trimer are useful for
CC inducing apoptosis in mammalian cells, by exposing mammalian cells
CC expressing a receptor selected from DR4 receptor and DR5 receptor to a
CC therapeutically effective amount of the Apo-2 ligand variant polypeptide,
CC Apo-2 ligand composition or Apo-2 ligand trimer. The mammalian cells are
CC colon or colorectal cancer cells. The Apo-2 ligand variant polypeptide,
CC the Apo-2 ligand composition or the Apo-2 ligand trimer is useful for
CC treating cancer (such as lung, breast, colon or colorectal cancer) or an
CC immune-related disease (such as arthritis or multiple sclerosis) in a
CC mammal, by administering to the mammal an effective amount of the Apo-2
CC ligand variant polypeptide, Apo-2 ligand composition or Apo-2 ligand
CC trimer. This sequence represents the native human Apo-2 ligand protein of
CC the invention.
XX
SQ Sequence 281 AA;
Query Match 100.0%; Score 1287; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGKGIACFLKEDDSYDNDDESMNSPCWQVQWQLRQLVRLMILTSEE 60
DB 39 TNELKQMDKYSGKGIACFLKEDDSYDNDDESMNSPCWQVQWQLRQLVRLMILTSEE 98

QY 61 TISTVQEKQNIPLVREGRGQVAAHITGTRGSNTLSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQNIPLVREGRGQVAAHITGTRGSNTLSPNSKNEKALGRKINSWESSR 158

QY 121 SGHSFSLNHLRNGELVIHEKGFYIYSQYFRFQBEIKENTKDKQWQYIYKTSYDP 180
DB 159 SGHSFSLNHLRNGELVIHEKGFYIYSQYFRFQBEIKENTKDKQWQYIYKTSYDP 218

QY 181 PILLKSGARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLKSGARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278

QY 241 LVG 243
DB 279 LVG 281

RESULT 39
ADC35202
ID ADC35202 standard; protein; 281 AA.
XX
AC ADC35202;
XX
XX 18-DEC-2003 (first entry)
XX
XX Human TNF ligand family member #10.
XX
XX human; tumor necrosis factor; TNF ligand; endokine alpha;
XX excessive bone resorption disorder; osteoporosis; Paget's disease;
XX arterial calcification.
XX
XX Homo sapiens.
XX
XX US2003100074-A1.
XX
XX 29-MAY-2003.
XX
XX 15-AUG-2002; 2002US-00218547.
XX
XX 16-AUG-2001; 2001US-0312542P.
XX
XX 30-OCT-2001; 2001US-0330761P.
XX
XX (YUGG/) YU G.
XX
XX

```
PA (NIJ/) NI J.
PA (ROSE/) ROSEN C A.
XX (NARD/) NARDELLI B.
PI Yu G, Ni J, Rosen CA, Nardelli B;
XX WPI; 2003-696072/66.
DR N-PSDB; ADC35201.
XX
XX New Endokine alpha gene useful for preparing a composition for treating a
PT disease associated with excessive or insufficient bone resorption e.g.,
PT osteoporosis, Paget's disease or arterial calcification.
XX
XX Disclosure; SEQ ID NO 20; 145pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule encoding a
CC tumour necrosis factor family ligand. A composition comprising the
CC isolated antibody or its fragment is used for treating an individual in
CC need of decreased level of endokine alpha activity. The endokine alpha
CC polypeptide present in a heterotrimeric complex is used for treating an
CC individual having a disorder associated with excessive bone resorption,
CC e.g. osteoporosis, Paget's disease or arterial calcification. Treating an
CC individual having a disorder associated with insufficient bone resorption
CC comprises administering an endokine alpha antagonist, which is the
CC antibody that binds specifically to endokine alpha polypeptide. The
CC present sequence represents the amino acid sequence of a tumour necrosis
CC factor family ligand.
XX
XX Sequence 281 AA;
SQ
Query Match 100.0%; Score 1287; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELQMDQKYSKSGIACFLKEDDSYDNDDESNMSPCWQVKQLRQLVRKMLRTSEE 60
DB 39 TNELQMDQKYSKSGIACFLKEDDSYDNDDESNMSPCWQVKQLRQLVRKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGQORVAAHITCTGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGQORVAAHITCTGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLNLHLRNGELVHEKGFYIYSQTYFRFOEIKENTKDKQMVQIYKYTSYD 180
DB 159 SGHSFLNLHLRNGELVHEKGFYIYSQTYFRFOEIKENTKDKQMVQIYKYTSYD 218
QY 181 PILLMKSARNSCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNSCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281
RESULT 40
ADD14080
ID ADD14080 standard; protein; 281 AA.
XX
XX AC ADD14080;
XX
XX 01-JAN-2004 (first entry)
XX
XX Human src biomarker polypeptide SEQ ID NO:269.
XX
XX predictor set; protein tyrosine kinase activity modulator;
KW protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic;
KW gene therapy; drug sensitivity; genetic profile; cancer; human.
XX
XX Homo sapiens.
XX
XX WO2003062395-A2.
XX
```

```
PD 31-JUL-2003.
XX
XX 17-JAN-2003; 2003WO-US001981.
XX
XX 18-JAN-2002; 2002US-0350061P.
XX
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.
XX
XX Huang F, Fairchild CR, Lee FY, Shaw P;
XX
XX WPI; 2003-636735/60.
XX
XX N-PSDB; ADD14676.
XX
XX New polynucleotides and polypeptides for predicting the activity of
PT compounds that interact with protein tyrosine kinases and/or protein
PT tyrosine kinase pathways.
XX
XX Claim 10; SEQ ID NO 269; 139pp; English.
XX
XX The present invention describes a predictor set comprising a plurality of
CC polynucleotides or polypeptides whose expression pattern is predictive of
CC the response of cells to treatment with a compound that modulates protein
CC tyrosine kinase activity or members of the protein tyrosine kinase
CC pathway. Also described: (1) predicting whether a compound is capable of
CC modulating the activity of cells, comprising obtaining a sample of cells,
CC determining whether the cells express a plurality of markers, and
CC correlating the expression of the markers to the compound's ability to
CC modulate the activity of the cells; (2) a plurality of cell lines for
CC identifying polynucleotides and polypeptides whose expression levels
CC correlate with compound sensitivity or resistance of cells associated
CC with a disease state; and (3) identifying polynucleotides and
CC polypeptides that predict compound sensitivity or resistance of cells
CC associated with a disease state, comprising subjecting the plurality of
CC cell lines to one or more compounds, analysing the expression pattern of
CC a microarray of polynucleotides or polypeptides, and selecting
CC polynucleotides or polypeptides that predict the sensitivity or
CC resistance of cells associated with a disease state by using the
CC expression pattern of the microarray. The polynucleotides and
CC polypeptides have cytostatic activities, and can be used in gene therapy.
CC The polynucleotides and polypeptides are useful in predicting the
CC activity of compounds that interact with protein tyrosine kinases and/or
CC protein tyrosine kinase pathways. These may be used in determining drug
CC sensitivity in patients to allow the development of individualized
CC genetic profiles which aid in treating diseases and disorders (e.g.
CC cancer) based on patient response at a molecular level. The present
CC sequence is used in the exemplification of the present invention.
XX
XX Sequence 281 AA;
SQ
Query Match 100.0%; Score 1287; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELQMDQKYSKSGIACFLKEDDSYDNDDESNMSPCWQVKQLRQLVRKMLRTSEE 60
DB 39 TNELQMDQKYSKSGIACFLKEDDSYDNDDESNMSPCWQVKQLRQLVRKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGQORVAAHITCTGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGQORVAAHITCTGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLNLHLRNGELVHEKGFYIYSQTYFRFOEIKENTKDKQMVQIYKYTSYD 180
DB 159 SGHSFLNLHLRNGELVHEKGFYIYSQTYFRFOEIKENTKDKQMVQIYKYTSYD 218
QY 181 PILLMKSARNSCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSARNSCSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281
```



```

RESULT 41
ADD19010
ID ADD19010 standard; protein; 281 AA.
XX
AC AC
XX
XX
DT DT
XX
DE DE
XX
XX human; disease state; cytostatic; antiinflammatory; ophthalmological;
KW antiarteriosclerotic; vulnerary; gene therapy;
KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
KW glucose transportation; catecholamine synthesis; iron transport;
KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
KW inflammatory condition; wound healing.
XX
XX Homo sapiens.
OS
XX
XX WO2003018621-A2.
PN
XX
XX 06-MAR-2003.
PD
XX
XX 23-AUG-2002; 2002WO-GB003892.
PF
XX
XX 23-AUG-2001; 2001GB-00020558.
PR
XX
XX 05-OCT-2001; 2001GB-00024037.
PR
XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
PA
XX
XX Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
PI
XX
XX WPI; 2003-290046/28.
DR
XX
XX N-PSDB; ADD19011.
DR
XX
XX New substantially purified polypeptide, useful for diagnosing or treating
PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
PT wound healing.
XX
XX Claim 25; SEQ ID NO 499; 424pp; English.
PS
XX
XX This invention relates to novel human genes and gene product which are
CC implicated in certain disease states. Compounds which modulate the
CC proteins of the invention may have cytostatic, antiinflammatory,
CC ophthalmological, antiarteriosclerotic or vulnerary activities. The
CC sequences of the invention may be useful for gene therapy. The invention
CC may be useful for diagnosing or treating a hypoxia-regulated condition,
CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
CC erythropoiesis, or the biological response to hypoxia conditions
CC including processes such as glycolysis, gluconeogenesis, glucose
CC transportation, catecholamine synthesis, iron transport or nitric oxide
CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
CC inflammatory conditions or wound healing. The present sequence is that
CC a disease related protein of the invention.
XX
XX Sequence 281 AA;
SQ
Query Match 100.0%; Score 1287; DB 7; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TNELKQMDKYSKSGIACFLKDDSYWDPNDEESNNSPCWQKQLRVKMLIRSEE 60
DB 39 TNELKQMDKYSKSGIACFLKDDSYWDPNDEESNNSPCWQKQLRVKMLIRSEE 98
QY 61 TISTVQEKQNTISPLVRERGQORVAHITGRGNTLTSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQNTISPLVRERGQORVAHITGRGNTLTSSPNSKNEKALGRKINSWESSR 158

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QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQYFQBEIKENTKNDKQWVYIKYTSYPD 180
DB 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQYFQBEIKENTKNDKQWVYIKYTSYPD 218
QY 181 PILMKSGARNSCWSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILMKSGARNSCWSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281
RESULT 42
ADE76953
ID ADE76953 standard; protein; 281 AA.
XX
XX ADE76953;
XX
XX 29-JAN-2004 (first entry)
XX
XX Human protein expressed in a liver disorder #32.
DE
XX
XX human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
KW tumour; liver; inflammatory disorder; immune response disorder;
KW high-throughput screening; differential gene expression; gene therapy.
XX
XX Homo sapiens.
OS
XX
XX US2003108871-A1.
PN
XX
XX 12-JUN-2003.
PD
XX
XX 30-JUL-2001; 2001US-00919039.
PF
XX
XX 28-JUL-2000; 2000US-0222113P.
PR
XX
XX (KASE/) KASER M R.
PA
XX
XX Kaser MR;
PI
XX
XX WPI; 2004-031227/03.
DR
XX
XX N-PSDB; ADE76952.
DR
XX
XX Composition comprising several cDNAs that are differentially expressed in
PT treated human C3A liver cell cultures, useful for treating liver
PT disorders.
XX
XX Claim 1; SEQ ID NO 118; 41pp; English.
PS
XX
XX The invention relates to a composition comprising several cDNAs that are
CC differentially expressed in a liver disorder. The composition is useful
CC for treating liver disorder such as hyperlipidaemia, hypertension, type
CC II diabetes, tumours of the liver and disorders of the inflammatory and
CC immune response. The composition is useful for a high-throughput method
CC of screening several molecules or compounds to identify a ligand which
CC specifically binds a cDNA. A protein encoded by the cDNA is useful for a
CC high-throughput method for using a protein to screen several molecules or
CC compounds to identify at least one ligand which specifically binds the
CC protein which involves combining the protein encoded by the cDNA with
CC several of molecules or compounds under conditions to allow specific
CC binding, and detecting specific binding between the protein and a
CC molecule or compound, therefore identifying a ligand which specifically
CC binds the protein. The composition is useful for detecting and
CC quantifying differential gene expression, can be used in gene therapy, to
CC formulate prognosis and to design a treatment regimen and to monitor the
CC efficacy of treatment. The present sequence represents the amino acid
CC sequence of a protein encoded by a cDNA differentially expressed in a
CC liver disorder.
XX
XX Sequence 281 AA;
SQ

```

Query Match 100.0%; Score 1287; DB 8; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.3e-117;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TNELKQMDKYSGGIACFLKEDDSYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEE 60
Db |||||
Qy 39 TNELKQMDKYSGGIACFLKEDDSYWDPNDEESMNSPCWQVQWQLRQLVRKMLRTSEE 98
Db |||||
Qy 61 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db |||||
Qy 99 TISTVQEKQONISPLVRERGQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
Db |||||
Qy 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEBIKENTKDKQWQYIYKITSYPD 180
Db |||||
Qy 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEBIKENTKDKQWQYIYKITSYPD 218
Db |||||
Qy 181 PILLMKSARNSCWSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db |||||
Qy 241 LVG 243
Db |||||
Qy 279 LVG 281

Search completed: June 3, 2004, 11:35:43
Job time : 64 secs

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OM protein - protein search, using sw model

Run on: June 3, 2004, 08:53:00 ; Search time 22 Seconds
(without alignments)
570.232 Million cell updates/sec

Title: US-10-662-430-2_COPY_39_281
Perfect score: 1287
Sequence: 1 TNELKQMDKYSKGIACFL.....NEHLMDHDEASFFGAFVWG 243

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/2/iaa/5A COMB.pdp.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pdp.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pdp.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pdp.*
5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pdp.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1287	100.0	279	US-09-072-993C-3	Sequence 3, Appli
2	1287	100.0	281	US-08-670-354-2	Sequence 2, Appli
3	1287	100.0	281	US-08-584-031-1	Sequence 1, Appli
4	1287	100.0	281	US-08-780-496-1	Sequence 10, Appli
5	1287	100.0	281	US-08-883-086-10	Sequence 2, Appli
6	1287	100.0	281	US-09-320-424-2	Sequence 6, Appli
7	1287	100.0	281	US-09-333-593A-6	Sequence 11, Appli
8	1287	100.0	281	US-09-157-864-11	Sequence 2, Appli
9	1287	100.0	281	US-08-825-563-2	Sequence 66, Appli
10	1287	100.0	281	US-10-039-785-66	Sequence 2, Appli
11	1287	100.0	281	PCT-US96-10895-2	Sequence 11, Appli
12	988	76.8	253	US-09-320-424-11	Sequence 11, Appli
13	988	76.8	253	US-09-825-563-11	Sequence 13, Appli
14	988	76.8	256	US-09-320-424-13	Sequence 13, Appli
15	988	76.8	256	US-09-825-563-13	Sequence 7, Appli
16	930	72.3	177	US-08-105-343A-7	Sequence 6, Appli
17	863	67.1	291	US-08-670-354-6	Sequence 6, Appli
18	863	67.1	291	US-09-320-424-6	Sequence 6, Appli
19	863	67.1	291	US-09-825-563-6	Sequence 6, Appli
20	863	67.1	291	PCT-US96-10895-6	Sequence 6, Appli
21	850	66.0	161	US-09-565-423-7	Sequence 7, Appli
22	654	50.8	183	US-08-105-343A-8	Sequence 8, Appli
23	446	34.7	85	US-09-632-287A-12	Sequence 12, Appli
24	291	22.6	101	US-08-670-354-4	Sequence 4, Appli
25	291	22.6	101	US-09-320-424-4	Sequence 4, Appli
26	291	22.6	101	US-09-825-563-4	Sequence 4, Appli
27	291	22.6	101	PCT-US96-10895-4	Sequence 4, Appli

28	245.5	19.1	87	4	US-09-632-287A-13	Sequence 13, Appli
29	238.5	18.5	294	3	US-08-996-139-11	Sequence 11, Appli
30	238.5	18.5	294	3	US-08-995-659-11	Sequence 11, Appli
31	238.5	18.5	294	3	US-09-215-649A-11	Sequence 11, Appli
32	238.5	18.5	294	4	US-08-577-780-11	Sequence 11, Appli
33	238.5	18.5	294	4	US-08-577-800-11	Sequence 11, Appli
34	238.5	18.5	294	4	US-09-466-496-11	Sequence 11, Appli
35	238.5	18.5	294	4	US-09-871-856-11	Sequence 11, Appli
36	238.5	18.5	294	4	US-09-871-291-11	Sequence 11, Appli
37	238.5	18.5	294	4	US-09-877-650-11	Sequence 7, Appli
38	238.5	18.5	316	2	US-08-842-842-7	Sequence 2, Appli
39	238.5	18.5	316	3	US-08-989-362-2	Sequence 2, Appli
40	238.5	18.5	316	4	US-09-552-521C-2	Sequence 2, Appli
41	238.5	18.5	316	4	US-09-671-658A-2	Sequence 2, Appli
42	238.5	18.5	316	4	US-09-396-937-4	Sequence 4, Appli
43	238.5	18.5	316	4	US-09-396-937-6	Sequence 4, Appli
44	235.5	18.3	317	3	US-08-996-139-13	Sequence 13, Appli
45	235.5	18.3	317	3	US-08-995-659-13	Sequence 13, Appli

ALIGNMENTS

RESULT 1
US-09-072-993C-3
; Sequence 3, Application US/09072993C
; Patent No. 6346388
; GENERAL INFORMATION:
; APPLICANT: Michael R. Brigham-Burke
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030
; CURRENT APPLICATION NUMBER: US/09/072,993C
; CURRENT FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 279
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-072-993C-3
Query Match 100.0%; Score 1287; DB 4; Length 279;
Best Local Similarity 100.0%; Pred. No. 2.2e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TNELKQMDKYSKGIACFLKEDDSYWDPNDEESMNSPCWQVQWQLRQVLRKMLRTSEE	60
Db	37	TNELKQMDKYSKGIACFLKEDDSYWDPNDEESMNSPCWQVQWQLRQVLRKMLRTSEE	96
QY	61	TISTVQEQKQNISPLVRRGPGORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR	120
Db	97	TISTVQEQKQNISPLVRRGPGORVAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR	156
QY	121	SGHSFLSNLHNLNGELVTHKGFYIYSQTVFRFOEEKENTKNDKQWQVYIKYTSYD	180
Db	157	SGHSFLSNLHNLNGELVTHKGFYIYSQTVFRFOEEKENTKNDKQWQVYIKYTSYD	216
QY	181	PILLMKSAFNSCWSDAEYGLYSYIYGGIFELKENDRIFVSVTNHLLMDHDEASFFGAF	240
Db	217	PILLMKSAFNSCWSDAEYGLYSYIYGGIFELKENDRIFVSVTNHLLMDHDEASFFGAF	276
QY	241	LVG 243	
Db	277	LVG 279	

```

RESULT 2
US-08-670-354-2
; Sequence 1, Application US/08670354
; Patent No. 5763223
; GENERAL INFORMATION:
; APPLICANT: Steven R. Wiley and
; APPLICANT: Raymond G. Goodwin.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/670,354
; FILING DATE: 25-JUN-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-670-354-2

Query Match 100.0%; Score 1287; DB 1; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE 98
QY 61 TISTVQEKQNIPLVREGRQPVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQNIPLVREGRQPVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHNLNGELVTHEKGFYIYSQTVFRQEEIKENTKNDKQVQIYKYTSYD 180
DB 159 SGHSFLSNLHNLNGELVTHEKGFYIYSQTVFRQEEIKENTKNDKQVQIYKYTSYD 218
QY 181 PILLMKSGNSCKSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSGNSCKSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 3
US-08-584-031-1
; Sequence 1, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; TITLE OF INVENTION: APO-2 LIGAND
; FILE REFERENCE: 11669.22US03
; CURRENT APPLICATION NUMBER: US/08/584,031A
; CURRENT FILING DATE: 1996-01-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-584-031-1

Query Match 100.0%; Score 1287; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCQVQWQLRQLVRKMLRTSEE 98
QY 61 TISTVQEKQNIPLVREGRQPVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQNIPLVREGRQPVAAHITGTRGSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHNLNGELVTHEKGFYIYSQTVFRQEEIKENTKNDKQVQIYKYTSYD 180
DB 159 SGHSFLSNLHNLNGELVTHEKGFYIYSQTVFRQEEIKENTKNDKQVQIYKYTSYD 218
QY 181 PILLMKSGNSCKSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLMKSGNSCKSKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 4
US-08-780-496-1
; Sequence 1, Application US/08780496
; Patent No. 6045048
; GENERAL INFORMATION:
; APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin Kim
; TITLE OF INVENTION: Apo-2 Ligand
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/780,496
; FILING DATE: 08-Jan-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0978P1

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5416
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-780-496-1

Query Match 100.0%; Score 1287; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGQORVAHAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGQORVAHAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYDP 180
DB 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYDP 218
QY 181 PILLKMSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLKMSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 5
US-08-883-086-10
Sequence 10, Application US/08883086
Patent No. 6171787
GENERAL INFORMATION:
APPLICANT: WILEY, STEVEN
TITLE OF INVENTION: MEMBER OF THE TNF FAMILY USEFUL
TITLE OF INVENTION: FOR TREATMENT AND DIAGNOSIS OF DISEASE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/883,086
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Foremski, Priscilla E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 6134.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-937-0378
TELEFAX: 847-938-2623
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 6171787e
US-08-883-086-10

Query Match 100.0%; Score 1287; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGQORVAHAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGQORVAHAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYDP 180
DB 159 SGHSFLSNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQWQVIYKYTSYDP 218
QY 181 PILLKMSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
DB 219 PILLKMSARNSCWSDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 6
US-09-320-424-2
Sequence 2, Application US/09320424
Patent No. 6284236
GENERAL INFORMATION:
APPLICANT: Wiley, Steven R.
APPLICANT: Goodwin, Raymond G.
TITLE OF INVENTION: Cytokine that Induces Apoptosis
FILE REFERENCE: 2835-E
CURRENT APPLICATION NUMBER: US/09/320,424
CURRENT FILING DATE: 1999-05-26
EARLIER APPLICATION NUMBER: 09/190,046
EARLIER FILING DATE: 1998-11-10
EARLIER APPLICATION NUMBER: 09/048,641
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: 08/670,354
EARLIER FILING DATE: 1996-06-25
EARLIER APPLICATION NUMBER: 08/548,368
EARLIER FILING DATE: 1995-11-01
EARLIER APPLICATION NUMBER: 08/496,632
EARLIER FILING DATE: 1995-06-29
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 281
TYPE: PRT
ORGANISM: human
US-09-320-424-2

Query Match 100.0%; Score 1287; DB 3; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLKMLRTSEE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYWDPNDEESMNSPCWQVKQLRQVLKMLRTSEE 98
QY 61 TISTVQEKQONISPLVRERGQORVAHAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
DB 99 TISTVQEKQONISPLVRERGQORVAHAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158


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; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
; PRIOR APPLICATION NUMBER: 08/548,368
; PRIOR FILING DATE: 1995-11-01
; PRIOR APPLICATION NUMBER: 08/496,632
; PRIOR FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: human
US-09-825-563-2

Query Match      100.0%; Score 1287; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGIACFLKEDDSYWDNDDESMNSPCWQVQWLRLVRLMILRTSEE 60
Db 39 TNELKQMDKYSGIACFLKEDDSYWDNDDESMNSPCWQVQWLRLVRLMILRTSEE 98
QY 61 TISTVQEKQNIPLVREGRQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQNIPLVREGRQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVHKEGFYIYSQTYFRFQBEIKENTKDKQVQVYIKYTSYDP 180
Db 159 SGHSFSLNHLRNGELVHKEGFYIYSQTYFRFQBEIKENTKDKQVQVYIKYTSYDP 218
QY 181 PILLKMSARNSCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLKMSARNSCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
Db 279 LVG 281

RESULT 10
US-10-039-785-66
; Sequence 66, Application US/10039785
; Patent No. 6538938
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF550
; CURRENT APPLICATION NUMBER: US/10/039,785
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/369,860
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/331,310
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/331,044
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: 60/327,364
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: 60/323,807
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/309,176
; PRIOR FILING DATE: 2001-08-02

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; PRIOR APPLICATION NUMBER: 60/294,981
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: 60/293,473
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-039-785-66

Query Match      100.0%; Score 1287; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 2.2e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSGIACFLKEDDSYWDNDDESMNSPCWQVQWLRLVRLMILRTSEE 60
Db 39 TNELKQMDKYSGIACFLKEDDSYWDNDDESMNSPCWQVQWLRLVRLMILRTSEE 98
QY 61 TISTVQEKQNIPLVREGRQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 120
Db 99 TISTVQEKQNIPLVREGRQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWESSR 158
QY 121 SGHSFSLNHLRNGELVHKEGFYIYSQTYFRFQBEIKENTKDKQVQVYIKYTSYDP 180
Db 159 SGHSFSLNHLRNGELVHKEGFYIYSQTYFRFQBEIKENTKDKQVQVYIKYTSYDP 218
QY 181 PILLKMSARNSCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 240
Db 219 PILLKMSARNSCKDAEYGLYSIQGGIFELKENDRIFVSVTNEHLIDMDHEASFFGAF 278
QY 241 LVG 243
Db 279 LVG 281

RESULT 11
PCT-US96-10895-2
; Sequence 2, Application PC/TUS9610895
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation.
; TITLE OF INVENTION: Cytokine That Induces Apoptosis
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Anderson, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.5.2
; SOFTWARE: Microsoft Word, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10895
; FILING DATE: 25-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/496,632
; FILING DATE: 29-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/548,368
; FILING DATE: 01-NOV-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2835-WO
; TELECOMMUNICATION INFORMATION:

```


TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10895-2

Query Match 100.0%; Score 1287; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 2e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDESMNSPCWQVQKQLRQVRKMLRTSBE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDESMNSPCWQVQKQLRQVRKMLRTSBE 98
QY 61 TISVQEKQNIISPLVREGRPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 120
DB 99 TISVQEKQNIISPLVREGRPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 158
QY 121 SGHSFLNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQVQYIYKTSYD 180
DB 159 SGHSFLNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQVQYIYKTSYD 218
QY 181 PILLMKSARNCSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 240
DB 219 PILLMKSARNCSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 12
US-09-320-424-11
; Sequence 11, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; PRIOR FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-320-424-11

Query Match 76.8%; Score 988; DB 3; Length 253;
Best Local Similarity 78.9%; Pred. No. 2e-94;
Matches 194; Conservative 15; Mismatches 13; Indels 24; Gaps 2;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDESMNSPCWQVQK---WQLRQLVRKMLRT 57
DB 29 SDRMKQIEDKI-----EELSKIYHIENIARIKKLIGERTST 67
QY 58 SEETISTVQEKQNIISPLVREGRPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 117
DB 68 SEETISTVQEKQNIISPLVREGRPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 127
QY 118 SSRGSHSFLNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQVQYIYKTS 177
DB 128 SSRGSHSFLNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQVQYIYKTS 187
QY 178 YPDPILLMKSARNCSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 237
DB 188 YPDPILLMKSARNCSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 247
QY 238 GAFLVG 243
DB 248 GAFLVG 253

TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10895-2

Query Match 100.0%; Score 1287; DB 5; Length 281;
Best Local Similarity 100.0%; Pred. No. 2e-125;
Matches 243; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDESMNSPCWQVQKQLRQVRKMLRTSBE 60
DB 39 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDESMNSPCWQVQKQLRQVRKMLRTSBE 98
QY 61 TISVQEKQNIISPLVREGRPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 120
DB 99 TISVQEKQNIISPLVREGRPQVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 158
QY 121 SGHSFLNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQVQYIYKTSYD 180
DB 159 SGHSFLNLHRLNGELVIHEKGFYIYSQTYFRFOEIKENTKNDKQVQYIYKTSYD 218
QY 181 PILLMKSARNCSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 240
DB 219 PILLMKSARNCSKDAEYGLYSYQGGIFELKENDRIFVSVTNEHLIDMDHEASFF 278
QY 241 LVG 243
DB 279 LVG 281

RESULT 12
US-09-320-424-11
; Sequence 11, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; PRIOR FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 11
; LENGTH: 253
; TYPE: PRT
; ORGANISM: synthetic fusion
US-09-320-424-11

Query Match 76.8%; Score 988; DB 3; Length 253;
Best Local Similarity 78.9%; Pred. No. 2e-94;
Matches 194; Conservative 15; Mismatches 13; Indels 24; Gaps 2;

QY 1 TNELKQMDKYSKSGIACFLKEDDSYNDPNDDESMNSPCWQVQK---WQLRQLVRKMLRT 57
DB 29 SDRMKQIEDKI-----EELSKIYHIENIARIKKLIGERTST 67

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RESULT 14
US-09-320-424-13
; Sequence 13, Application US/09320424
; Patent No. 6284236
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/320,424
; EARLIER FILING DATE: 1999-05-26
; EARLIER APPLICATION NUMBER: 09/190,046
; EARLIER FILING DATE: 1998-11-10
; EARLIER APPLICATION NUMBER: 09/048,641
; EARLIER FILING DATE: 1998-03-26
; EARLIER APPLICATION NUMBER: 08/670,354
; EARLIER FILING DATE: 1996-06-25
; EARLIER APPLICATION NUMBER: 08/548,368
; EARLIER FILING DATE: 1995-11-01
; EARLIER APPLICATION NUMBER: 08/496,632
; EARLIER FILING DATE: 1995-06-29
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 13
; LENGTH: 256
; TYPE: PRT
; ORGANISM: synthetic fusion
; US-09-320-424-13

Query Match
Best Local Similarity 76.8%; Score 988; DB 3; Length 256;
Matches 194; Conservative 15; Mismatches 13; Indels 24; Gaps 2;

Qy 1 TNELKQMDKYKSGIACFLKEDDSYWDPNDESMNSPCWQVK---WQLRQLVRKMLRT 57
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 32 SDRMKQIEDKI-----BEILSKIYHIENEIARIKKGIGERTST 70

Qy 58 SEETISTVQEKQKQNIPLVREGRQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 117
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 SEETISTVQEKQKQNIPLVREGRQORVAAHITGTRGRSNTLSSPNSKNEKALGRKINSWE 130

Qy 118 SSRSCHSFLNLHRLNGELVIHEKGFYIYSQYFRFOBEIKENTKNDKQWQYIYKYS 177
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Search completed: June 3, 2004, 08:56:54
Job time : 23 secs

RESULT 15
US-09-825-563-13
; Sequence 13, Application US/09825563
; Patent No. 6521228
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Cytokine that Induces Apoptosis
; FILE REFERENCE: 2835-E
; CURRENT APPLICATION NUMBER: US/09/825,563
; CURRENT FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 09/320,424
; PRIOR FILING DATE: 1999-05-26
; PRIOR APPLICATION NUMBER: 09/190,046
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: 09/048,641
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 08/670,354
; PRIOR FILING DATE: 1996-06-25
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